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Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| 5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ა 5 | 34 | 33 | 32 | 31 | 30 |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------|
| 114 | 114 | 115.5 | 116 | 117 | 117.5 | 117.5 | 117.5 | 117.5 | 118.5 | 118.5 | 120 | 121 | 121 | 124.5 | 125 |
| 15.0 | 15.0 | 15,2 | 15.3 | 15.4 | 15.5 | 15.5 | 15.5 | 15.5 | 15.6 | 15.6 | 15.8 | 15.9 | 15.9 | 16.4 | 16.4 |
| 2437 | 828 | 1058 | 1549 | 1435 | 395 | 360 | 348 | 347 | 382 | 347 | 476 | 888 | 237 | 209 | 1964 |
| ۵ | N | N | N | N | N | N | Ŋ | N | N | 2 | N | N | N | N | N |
| \$42612 | T52046 | D82654 | T13940 | T32930 | 138741 | 138743 | I38744 | C48146 | В40858 | C40858 | T23213 | D84650 | T50984 | T15888 | T09059 |
| transmembrane prot | potassium channel | ankyrin-like prote | ankyrin - fruit fl | hypothetical prote | nuclear respirator | nuclear respirator | nuclear respirator | nuclear respirator | GA-binding protein | GA-binding protein | hypothetical prote | probable potassium | related to 26s pro | hypothetical prote | notch4 - mouse |

ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
C;Accession: JE0141; 159268; S39359; I59585; JC5679
R;Huang, C.G.; Deng, W.; Fu, J.L.
Chin. J. Biotechnol. 13, 105-107, 1997
A;Title: Molecular cloning and sequencing of P16 ink4 cDNA from hela cell.
A;Reference number: JE0141
A;Accession: JE0141 A;Gene: GDB:CDKN2A; CDK41; MLM; P16; INK4; MTS1; CMM2; CDKN2
A;Cross-references: GDB:335362; OMIM:600160
A;Map position: 9p21-9p21
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C;Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor A;Note: this sequence is corrected in reference 159268
R;Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;
Science 264, 436-440, 1994
A;Title: A cell cycle regulator potentially involved in genesis of many tumor types.
A;Reference number: 159585; MUID:94204645
A;Accession: 159585 R;Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994
A;Title: Mutations and altered expression of pl6INK4 in human cancer.
A;Reference number: 159268; MUID:95062202
A;Accession: 159268 C; Genetics: A;Cross-references: GB:S69804; NID:g546272; PIDN:AAD14048.1; PID:g4261748 C;Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 ki A;Title: A new regulatory motif in cell-cycle control causing specific inhibition of A;Reference number: S39359; MUID:94081956
A;Accession: S39359 A;Cross-references: GB:L27211; NID:g558656; PIDN:AAA92554.1; PID:g558657 A;Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925 R;Seriano, M.; Hannon, G.J.; Beach, D. Nature 366, 704-707, 1993 cyclin dependent kinase inhibitor - human N;Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor A; Molecule type: DNA
A; Residues: 51-152 < KAM> A; Status: translation not shown; translated from GB/EMBL/DDB A; Molecule type: mRNA A; Residues: 9-34,'V', 36-156 <SER> A;Status: preliminary A; Molecule type: DNA A; Residues: 1-152 < OKA> A; Status: translation not shown; translated from GB/EMBL/DDB. A;Experimental source: Hella cell A; Molecule type: mRNA A; Residues: 1-156 <HUA>

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R;Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Oncogene 11, 635-645, 1995

A;Title: Cloning and characterization of murine pl6INK4a and A;Reference number: 158352; MUID:95380169

A;Accession: 178845

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-130 <RESS

A;Cross-references: GB:S79252; NID:g1087092; PID:g1087093

C;Genetics: p15INK4b

C;Superfamily: unassigned ankyrin repeat proteins; ankyrin re
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                                                                                  A.Title: Growth suppression by p18, a p16(INK4/MTS1)- and p14
A; Reference number: A55479; MUID:95095079
A; Accession: B55479
A; Molecule type: mRNA
A; Residues: 1-138 <GUA>
A; Cross-references: GB:017075; NID:g639715; PIDN:AAC50075.1;
A; Experimental source: HeLa cells
R; Hannon, G.J.; Beach, D.
Nature 371, 257-261, 1994
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C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jul-2000
C;Accession: B55479; S47593; I81183; I52713
R;Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; J
Genes Dev. 8, 2939-2952, 1994
Nature 371, 257-261, 1994
A;Title: pl5(INKAB) is a potential effector of TGF-beta-induced A;Reference number: S47593; MUID:94359613
A;Accession: S47593
A;Molecule type: mRNA
A;Residues: 1-19, 'TP', 22, 24-31, 'HSW', 35-138 <HAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000
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99.38;
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Pred. No. 1.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 529; DB 2;
Pred. No. 2.4e-43;
4; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                     and p14(INK4B/MTS2)-related
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                                                                                                                                              PID:g639716
                                                                              cell
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                                                                              cycle arrest.
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p16INK4a - mouse
C; Species: Mus sp. (m
C; Date: 26-Jul-1996 #
C; Accession: I58352
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A;Title: Deletion of p16 and p15 genes in br A;Reference number: I52713; MUID:95079408
A;Accession: I52713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L36844; NID:g556197; PIDN:AAA50282.1; PID:g556198
A;Experimental source: HaCaT cells
R;Kamb, A; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 9p21-9p21
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C;Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 53-138 < KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: 181183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, Science 264, 435-440, 1994
A;Title: A cell cycle regulator potentially involved in genesis CA;Reference number: I59585; MUID:94204645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:CDKN2B;
A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-52 < RE
                                                                                                                                                                                                                    A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-167 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
158352
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                                                                                                                                                                                                                                                                           Oncogene 11, 635-645, 1995
A;Title: Cloning and characterization of murine pl6INK4a and A;Reference number: 158352; MUID:95380169
A;Accession: 158352
                                                                                                                                                                                                                                                                                                                                       R;Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, Oncogene 11, 635-645, 1995
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                                                                                                                                     C; Superfamily: unassigned
                                                                                                                                                        A; Gene: p16INK4a
                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
                                           Query Match 60.7
Best Local Similarity 63.7
Matches 98; Conservative
                                                                                                                                                                                   Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLR 123
MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
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                                                                                                                                                                                                   <res>
s: GB:S79251; NID:g1087090; PID:g1087091
                                                                                                                                                                                                                                                                                                                                                                                                                   (mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:S75756; NID:g861470; PIDN:AAD14186.1; PID:g4261886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.7%;
                                                               60.7%;
63.2%;
                                                                                                                                            ankyrin repeat proteins; ankyrin repeat homology;
                                             16;
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Pred. No. 1.2e-42;
4; Mismatches 14
                                                                 Score 461.5; DB 2; Pred. No. 8.5e-37;
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                                                 Mismatches
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er, D.D.; Papadopoulos, N.; Ma:
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                                                                                    Length
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C;Accession: A57379
C;Accession: A57379
RRHital, H.; Roussel, M.F.; Rato, J.Y.; Ashmun, R.A.; Sherr, C.J.
Mol. Cell. Biol. 15, 2672-2681, 1995
A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cy.
A;Reference number: A57379; MUID:95257948
A;Accession: A57379
A;Status: preliminary
A;Kolecule type: mRNA
A;Residues: 1-166 (HIR)
A;Cross-references: GB:U19597; NID:g790568; PIDN:AAC52194.1; PID:g790569
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
A57378
cyclin-dependent kinase inhibitor p19 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. Mol. Cell. Biol. 15, 2682-2688, 1955
A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor A;Reference number: A57378; MUID:95257949
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C;Keywords: cell cycle control
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Best Local
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                                       δ
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                                   DWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVRAGTLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGA 64
DRLSGARARGDVQEVRRLLHRELYHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNV 69
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                                                                                          32.8%;
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                                                                            18;
                                                               Score 249; Pred. No. 1.5e-18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 258; DB 2;
Pred. No. 2.1e-17;
7; Mismatches 62
                                                                        > 249; DB 2; I
. No. 1.5e-16;
ismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                     08-Feb-1996 #text_change 20-Sep-1999
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R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. Mol. Cell. Biol. 15, 2682-2688, 1995
A;Title: Identification of human and mouse p19, a novel CDK4 and A;Reference number: A57378; MUID:95257949
A;Accession: B57378
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
B57379
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C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                    CDK4/CDK6 inhibitor p18 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homolo
                                                                                                                                      A;Cross-references: GB:U19596; NID:g790566; PIDN:AAC52193.1; PID:g790567 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homolo C;Keywords: cell cycle control
                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-168 <HIR>
                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: B57379
                                                                                                                                                                                                                                                                                                                             R;Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J. Mol. Cell. Biol. 15, 2672-2681, 1995
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A; Residues: 1-166 < CHA>
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                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                             A; Title: Novel INK4 proteins,
                                                                                                                                                                                                                                                                                                                                                                      C; Accession: B57379
                   Query Match
Best Local Similarity 40.3
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Best Local Similarity
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2 EPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QD-ASGTSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESDLHHRDASGLTPLELARQRGAQNL-MDILQGHMMIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL-- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RAAAGGT-----RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                     proteins, p19 and p18, are specific inhibitors A57379; \mbox{MUID:}95257948
                                                           30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.1%; Score 244; DB 2; 1
43.7%; Pred. No. 4.6e-16;
tive 18; Mismatches 53;
                                         22;
                                     Score 231.5; DB 2
Pred. No. 7.2e-15;
2; Mismatches 6(
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                                                                               DB 2;
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                                         60;
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                                         Indels
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                                         Gaps
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EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGAN 62

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RESULT 9
A55479
CDK6 inhibitor p18 - human
CX6 inhibitor p18 - human
N;Alternate names: cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent kinase
CX5pecies: Homo sapiens (man)
CX5pecies: Homo sapiens (man)
CX50Ate: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Sep-1999
CXACCESSION: A55479
CXACCESSION: A55479
CXACCESSION: A55479
CXACCESSION: A55479; MUID:95095079
A;Accession: A55479; MUID:95095079
A;Accession: A55479; MUID:95095079
A;Accession: A55479; MUID:95095079
A;Accession: A55479; MUID:95095079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pl5INK4B protein - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C:Accession: I52720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GDB:CDKN2C
A;Cross references: GDB:594931
A;Cross references: GDB:594931
A;Map position: lp32-lp32
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C;Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δõ
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                                                                                                                                                                       C;Genetics:
A;Gene: p151NK4B
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
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                   QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                R; Knapek, D.F.;
Cancer Res. 55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-41 <RES>
                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                           A; Cross-references:
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Best Local :
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.sidues: 1-168 <GUA>
ross-references: GB:U17074; NID:g639713; PIDN:AAC50074.1; PID:g639714
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                      44 MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLD
                                                                     Local Similarity
les 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGAN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDLKD-RTGFAVIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEF 121
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56;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Serrano, M.; Beach, D.; Trono, D.; Walker, C.L. 1607-1612, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                       Conservative
                                                                                                                                                                                                                                                             GB:S77734; NID:g99871
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                                                                                           27.5%;
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                                                                  Score 209; DB Pred. No. 2.1e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDB
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                                                                                           DB 2;
.1e-13;
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                        84
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                                                                       Gaps
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A;Title: 440-kD ankyrinB: structure of the major developmentally regulated domain A;Reference number: A49462; MUID:94075409
A;Recession: A49462
A;Status: preliminary: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:226634; NID:9406287; PIDN:CAA81387.1; PID:9406288 R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.

J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal A;Reference number: A39643; MUID:91302466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
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N;Contains: ankyrin 2, short form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1993 A;Reference number: 837431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 463-474, PE', 477-495 < TSE>
A; Residues: 463-474, PE', 477-495 < TSE>
A; Cross-references: GB: M37123; NID: 9178647; PIDN: AAA62828.1; PID: 9178648
A; Cross-references: GB: M37123; NID: 9178647; PIDN: AAA62828.1; PID: 9178648
A; Cross-references: GB: M37123; NID: 9178647; PIDN: AAA62828.1; PID: 9178648
J. Cell Biol. 123, 1463-1473, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Isolation and chromosomal localization A;Reference number: A40334; MUID:92009921 A;Accession: A40334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-2077 <OT1>
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                                                                                                                                                                                                                                                                                                                                                         F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status pred
F;2-1443,3585-3924/Product: ankyrin 2, short form #status pred
                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: ankyrin; ankyrin repeat C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Tse, W.T.; Menninger,
Genomics 10, 858-866, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1443, 3585-3924 <OTT>
A; Cross-references: EMBL: X56958
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                             F;496-528/Domain:
                                                 F;463-495/Domain:
                                                                         F;430-462/Domain:
                                                                                                  F;397-429/Domain:
                                                                                                                        F;364-396/Domain:
                                                                                                                                                 F;331-363/Domain:
                                                                                                                                                                     F;298-330/Domain:
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                                                                                                                                                                                                                                                                  F; 162-190/Domain:
                                                                                                                                                                                                                                                                                           F;129-161/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                    F;96-128/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                                       F;63-95/Domain: ankyrin repeat homology <AN01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 4q25-4q27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: ANK2
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A; Residues: 1-3924 <R
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       F;529-561/Domain:
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    repeat
                             repeat
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ice form; ankyrin-B; brain ankyrin; non-erythro
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nonerythroid

ankyrin Lux,

S.E.; gene ₩a

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F;562-594/Dymain: a
F;595-627/Domain: a
F;628-660/Domain: a
F;661-693/Domain: a
F;664-726/Domain: a
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F;440-472/Domain: ankyrin r
F;473-505/Domain: ankyrin r
F;506-538/Domain: ankyrin r
F;539-71/Domain: ankyrin r
F;539-64/Domain: ankyrin r
F;539-64/Domain: ankyrin r
F;638-670/Domain: ankyrin r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Birkenmeler, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E. J. Biol. Chem. 268, 9533-9540, 1993 A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are four A;Reference number: S37771; MUID:93252825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1848 <BIR>
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C;Species: Mus musculus (house mouse)
C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
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F;760-792/Domain:
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        Query Match
Best Local Similarity
Matches 51; Conser
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;407-439/Domain:
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Best Local S
Matches 48
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147-175/Domain: ankyrin repeat homology <an04>
147-175/Domain: ankyrin repeat homology <an05>
208/Domain: ankyrin repeat homology <an05>
241/Domain: ankyrin repeat homology <an06>
242-274/Domain: ankyrin repeat homology <an08>
275-307/Domain: ankyrin repeat homology <an08>
308-340/Domain: ankyrin repeat homology <an08>
311-373/Domain: ankyrin repeat homology <an08>
341-373/Domain: ankyrin repeat homology <an08-3>
341-373/Domain: ankyrin
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           Conservative
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34.7%;
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homology
  Score 137.5; DB 2;
Pred. No. 9.7e-05;
7; Mismatches 68;
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Pred. No. 2.5e-06;
B; Mismatches 59
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                                                     1848;
  11;
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F;106-138/Domain: ankyrin repeat homology <annonable f;139-167/Domain: ankyrin repeat homology <annotable f;139-167/Domain: ankyrin repeat homology <annotable f;168-200/Domain: ankyrin repeat homology <annotable f;201-233/Domain: ankyrin repeat homology <annotable f;201-233/Domain: ankyrin repeat homology <annotable f;204-266/Domain: ankyrin repeat homology <annotable f;201-239/Domain: ankyrin repeat homology <annotable f;201-239/Domain: ankyrin repeat homology <annotable f;301-332/Domain: ankyrin repeat
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F;762-794/Domain:
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C;Superfamily: ankyrin; ankyrin I
C;Keywords: alternative splicing
F;40-72/Domain: ankyrin repeat h
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F;465-497/Domain:
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A; Residues: 1-1862 < RI
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R;White, R.A.; Birk
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
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Best Local Similarity
620 YGGSANAESVQGVTPLHLAAQEGHTEM 646
                                                                      123
                                                                                                                                       563
                                                                                                                                                                                                                                                      503 LHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 KNGLT-PLHVAVHHNNLDIVKLLLPRGGS--PHSPAWNGYTPLHIAAKQNQIEVARSLLQ 627
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                                                                                                                                                                                  PATLTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL--
                                                                ~~-RAAAGGTRGSNHARIDAAEGPSDI 146
                                                                                                                            KNGLT-PLHVAVHHNNLDIVKLLLPRGGS--PHSPAWNGYTPLHIAAKQNQIEVARSLLQ
                                                                                                                                                                                                                                                                                                                   LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD
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34.7%;
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homology <AN13>
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homology <AN15>
                                                                                                                                                                                                                                                                                                                                                                                   Score 137.5; DB 2;
Pred. No. 9.8e-05;
7; Mismatches 68;
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ankyrin 1, erythrocyte splice form 3 - human
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N;Contains: ankyrin 2.2, erythrocyte
C;Species: Homo sapiens (man)
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C;Accession: B35049
                                                                                                                            RESULT
A35049
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A; Cross-references: GDB:118737; OMIM:182900
Ap position: 8p11.2-8p11.2
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A;Title: cDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370
A;Accession: B35049
ankyrin 1* erythrocyte splice form 2 - human N;Allernate, names: ankyrin 2.1, erythrocyte; N;Contains: ankyrin 2.2, erythrocyte C;Species: Hómo sapiens (man)
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F;601-633/Domain:
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A;Molecule type: mRNA
A;Residues: 1-1856 <LAM>
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F; 667-699/Domain:
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;502-534/Domain:
;535-567/Domain:
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Meywords: alternative splicing
2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
52; Conserv
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in repeat homology <anu0>
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in repeat homology
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Pred. No. 0.00023;
5; Mismatches 69;
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Search completed: Job time: 83 sec

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R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990 A;Title: cDNA sequence for human erythrocyte ankyrin. A;Reference number: A35049; MUID:90175370 A;Accession: A35049
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C;Accession: A35049
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F;304-336/Domain:
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F;205-237/Domain:
F;238-270/Domain:
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C;Keywords: alternative splicing; cytos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:118737; OMIM:182900
A;Map position: 8p11 2-8p11.2
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A;Residues: 1-1880 <LAM>
A;Cross-references: GB:M28880
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F;469-501/Domain:
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Best Local Similarity
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| 0; PubMed=975.9 g L., Lee J.O | 2 FROM N.A. PubMed=815: A., Weaver:E., tockert E., ulator poter ulator poter 40(1994). FROM N.A. PubMed=862; PubMed=862; Parry D., 6CDKN2 expre 6CDKN2 expre nd senescen 16:859-867(1 | o, Last sen 1, Last an 1 rast 4 inh pressor 1)). Chordata; Chordata; Primates; primates; ubMed=8259; G.J. neacl otif in Beacl otif in Beacl otif in DCDK4.", | DARD; | 2318 740 414 500 1178 668 1454 708 461 605 603 |
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VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT.

MEDLINE-96121580; PubMed-8595405;

Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,

Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;

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cell lung carcinomas.";
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"Somatic mutations of the MTS (multiple
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MEDLINE-97472457;
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VARIANTS MELANOMA GLY-59; TYR-84; TRP-87 AND TRP-101.

MEDDLINE-20332815; Pubmed-10874641;
A Ruiz A., Puig S., Malvehy J., Lazaro C., Lynch M., Gimenez-Ar Puig L., Sanchez-Conejo J., Estivill X., Castel T.;
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C -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS COLORS AND COLLD ACT AS A NEGATI REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.

C -!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
C -!- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION WIDE RANGE OF TISSUES.

C -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDE
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Hum. Mol. Genet
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-!- SIMILARITY: CONTAINS 4 ANK REPEATS
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Gretarsdottir S., Olafsdottir G.H., Bor
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16-OCT-2001 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B)
                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           MEDLINE=97322242; PubMed=9178896;
Malumbres M., de Castro I., Santos J., Melendez B.,
Serrano M., Pellicer A., Fernandez-Piqueras J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996
InterPro; IPR002110; ANK, Pfam; PF00023; ank; 3. SMART; SM00248; ANK; 1.
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J X DBA;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95380169; PubMed=7651726;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDKN2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                         TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
INDUCTION: BY TGF-BETA.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                            ween the Swiss Institute of Bioinformatics are European Bioinformatics Institute. There are
                                                                                                                                                                     SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                           SIMILARITY).
SUBUNIT: HETERODIMER OF P14 WITH
                                                                                                                                                                                                                                                FUNCTION: INTERACTS
POTENTIAL EFFECTOR C
                               MGI:104737;
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                                                                                                                                                                                 INHIBITORS.
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                                        U66085; AAB39833.1;
U66084; AAB39833.1;
P42771; 1BI7.
                                                                                                                 non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 34, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Rodentia;
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99.3%;
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Pred. No. 1.2e-65;
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                                                                                             (See http://www.isb-sib.ch/announce/
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rr C.J., Serrano
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RESULT
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Matches
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                                                                                                                                                                                                                                                                                      CDN5_RAT P55272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDKN2B OR INK4.

Rattus norvegicus (Rat).

Eukaryota, Metazoa; Chordata;

Mammalia; Eutheria; Rodentia;

NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
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PROSITE; PS50297; ANK_REP_REGION; 1
Cell_cycle; Anti-oncogene; Repeat; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B)
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01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hino O., Kobayashi E., Hirayama
Tsuchiya H., Kikuchi Y., Mitani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96001392; PubMed=7546221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchiya H., Kikuchi Y., Mitani H.; Molecular genetic basis of renal car model of tuberous sclerosis (Tsc2)."; Mol. Carcinog. 14:23-27(1995).
                                                 the European Bioinformatics Institute. The serious of the serious as long use by non-profit institutions as long
                                                                                                                                -!- SIMILARITY: CONTAINS 4 ANK REPEATS
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                                                                                                                                                          SUBUNIT: HETERODIMER OF P14 WITH CDK4.
ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTER ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTER INITIATION CODONS IN THE SAME READING FRAME.
TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS A TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPEN
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                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 88.1
106; Conservative
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ANK 3.
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Pred. No. 3
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                   http://www.isb-sib.ch/announce/
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T.,
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AAB35360.1;

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Matches
                                               SEQUENCE OF 53-138 FROM N.A.
SEQUENCE OF 53-138 FROM N.A.
MEDLINE-94204645; PubMed-8153634;
MEDLINE-94204645; N.A., Weaver-Feldhaus (Kamb A., Gruis N.A., Weaver E., Day R.S.
                                                                                               Nature
[3]
                                                                                                                                                               CDK6 inhibitor, correlates with wild-type prb function."; [2]
                                                                                                                                                                                       MEDLINE-95095079; PubMed-8001816; Guan K.-L., Jenkins C.W., Li Y., Matera G.A., Xiong Y.; "Growth suppression by p18, a p16
                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-94359613;
                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B)
                                                                                                                                                                                                                                                                                                                                              CDN5_HUMAN P42772;
                  Science 264:436-440(1994).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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REPEAT
VARIANTS LUNG ADENOCARCINOMA
                                                                                                                          "p15INK4B is a
                                                                                                                                    Hannon G.J.,
                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                       CDKN2B OR MTS2.
                                                                                                                                                                                                                                                                                                                                                                  HUMAN
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS50088; ANK_REPEAT; 1.
PROSITE: PS50297; ANK_REP_REGION; 1.
Cell cycle: Anti-concoccus.
                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Q60773;
                                                                                                       371:257-261(1994).
                                      cycle
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1AP7
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                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.9%;
                                    potentially
                                                                                                                        effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; ANK repeat; Alternative initiation. CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LONG ISOFORM.

CYCLIN-DEPENDENT KINASE 4
SHORT ISOFORM.
FOR SHORT ISOFORM.
ANK 1.
ANK 2.
ANK 3.
ANK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
GLU-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 524; DB 1
Pred. No. 1e-43;
5; Mismatches
                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC45B21FA69FAD92 CRC64;
                                                                                                                                                                                                          Nichols M.A.,
                                                                                                                         0f
AND
                                    involved in
                                                       J., L
                                                                                                                         TGF-beta-induced
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                                                       Liu Q., Ha
I, Johnson
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                                                                                                                                                                                                           Wu X.,
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                                    genesis
                                                                 Harshman
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                                                                                                                       cell cycle
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                                   of many tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     127
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RESULT
CDN2_M
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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EMBL; L36844; AAA502
EMBL; S69805; AAD140
HSSP; P42771; 1BI7.
                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor A (CDK4I)
CDKN2A OR P16INK4A.
Mus musculus (Mouse Fukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                      MOUSE
                                                                                            P51480;
                                                                                                       CDN2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: INTERACTS STRONGLY WITH CDK4
POTENTIAL EFFECTOR OF TGF-BETA INDUCED
-!- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
-!- DISEASE: CDKN2B MUTATIONS ARE INVOLVED
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95188190; PubMed=7882351;
Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A.,
Demetrick D.J., Serrano M., Hannon G.J., Shiseki M.,
Xiong Y., Beach D.H., Yokota J., Harris C.C.;
"Mutations in the p161MK4/MTS1/CDKN2, p151NK4B/MTS2,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50088; ANK_REPEAT; FAL
PROSITE; PS50297; ANK_REP_REGION;
Cell cycle; Anti-oncogene; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content use by non-brokent is not removed. Usage by armodified and this statement is not removed. Usage by armodified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHIBITORS.
-!- SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primary and metastatic lung cancer.";
Cancer Res. 55:1448-1451(1995).
                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK.
                                                                                                                                                                                                 124 AAAG 127
                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                          14 SDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSARVAELLLLHGAEPN
                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                      CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLR 123
                                                                                                                                                                        TATG
                                                                                                                                                                                                                         CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLR
                                                                                                                                                                                                                                                                                                    SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPN
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13 39
73 103
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               (Mouse)
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                                                                                                         STANDARD;
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 Chordata;
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85.5%;
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A -> V (IN LUNG ADENOCARCINOMA).
/FTId-VAR_001449.
SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
QLL -> HSW (IN REF. 2).
MICOLOFFBDFA6FEAD21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; ANK repeat;
                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                         Score 522; DB 1;
Pred. No. 1.7e-43;
Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G
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ANK 2.
                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                       167
 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions
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                                      (P16-INK4) (P16-INK4A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disease mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDK6.
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                                                                                                                                                                                                                                                                                                                                                    Length 138
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                                                                                                                                                                                                                                                                                                                            Indels
 Euteleostomi;
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Zariwala
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                                                                                             CDN2_MONDO
                                                                                                            RESULT
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15-JUL-1999 (Rel.
15-JUL-1999 (Rel.
16-OCT-2001 (Rel.
Cyclin-dependent k
                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D. Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; "Cloning and characterization of murine pl6INK4a and pl5INK4b Oncogene 11:635-645(1995).

-i- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.

PROSITE; PS50297; ANK_REP_REGION; 1.

Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.

CHAIN 1 167 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,

CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,

CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK. Pfam; PF00023; ank; 3. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                             CDN2_MONDO 077617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95380169; PubMed=7651726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:104738; Cdkn2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L76150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                           y Match
                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INHIBITORS.
SIMILARITY: CONTAINS 2 ANK REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTAINED CDK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6
                                                                                                                                                                                      YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                   EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                               {\tt MESAADRLA-RAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHVAALLLNYGALLENGER}
                                                                                                                                                       YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        060773;
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     43
35
101
167
(Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
ndent kinase 4 inhibitor A (CDK4I)
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      130 A
17870 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                           60.7%;
63.2%;
                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                           Score 461.5; DB 1
Pred. No. 1.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR SHORT ISOFORM ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHORT ISOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                         88C4588A105ECB8F CRC64;
                                                                                                                                                                                                                                                                                                                                              Mismatches
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There are no restrictions
ong as its content is in
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   (P16-INK4) (P16-INK4A)
                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                        _HUMAN STANDARD; PRT; 166 AA P.55273; Q13102; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update Cyclin-dependent kinase 4 inhibitor D (P19-
                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Didelphimorphia; Didelphidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Tumor suppressor CDKN2A). CDKN2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherburn T.E., Gale J.M., Submitted (MAY-1998) to t
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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or send an email to license@isb-sib.ch).
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                                                             CDKN2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
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                                                                                                                                                                                                                                                                                                                 4 SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INTITATION CODONS IN THE SAME READING FRAME.
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SIMILARITY: CONTAINS 3 ANK REPEATS.
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SHORT ISOFORM.
FOR SHORT ISOFORM
ANK 1.
ANK 2.
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Pred. No. 2e-32;
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                                                                           update)
(P19-INK4D).
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SEQUENCE FROM N.A.

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MEDLINE-96362662; PubMed-8741839;

Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Nob-
Zariwala M., Matera A.G., Xiong Y.;

"Isolation and characterization of p19INK4d, a p

RT specific to CDK6 and CDK4.";

Phol. Cell 7:57-70(1996).
             EMBL; U49399; AAB03772.1; -. EMBL; U20498; AAA85436.1; -. EMBL; U40343; AAB18139.1; -. EMBL; AF061327; AAC27450.1; -EMBL; AF044171; AAD07320.1; -PDB; 1B18; 16-FEB-99.
                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of human cyclin-dependent kinase inhibitor p19(INK4d): comparison to known ankyrin-repeat-containing structures and implications for the dysfunction of tumor suppressor p16(INK4a).", Structure 6:1279-1290(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.; "Structural basis for inhibition of the cyclin-dependent kinase Cdk6 "Structural busis for inhibition of the cyclin-dependent kinase Cdk6 "Structural Businessor pl6INK4a.";
                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baumgartner R., Fernandez-Catalan C., Winoto A., Huber
Holak T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=98455510; PubMed=9782052;
                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS
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Chan F.K.M., Zhang J., Cheng L., Shapir
"Identification of human and mouse p19,
inhibitor with homology to p16ink4.";
Mol. Cell. Biol. 15:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.", E_{\rm L} . J. Cancer 80:295-300(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishop D.T.;
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Okuda T., Hirai H., Valentine V.A., Shui
Lahti J.M., Sherr C.J., Downing J.R.;
"Molecular cloning, expression pattern,
of human CDKNDD/INK4d, an inhibitor of contains of the contains of th
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                   INHIBITORS.
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                                                                                        ; AAB03772.1; -.; AAA85436.1; -.; AAB18139.1; -.
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TO THE CDKN2 FAMILY
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RESULT 8
CDN7_MOUSE
ID CDN7_MOUSE
AC 060773; 060;
DT 01-NOV-1997
DT 01-NOV-101
CR CMammalia; EN
COC Mammalia; E
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Best Local
                                                                                                       STRUCTURE BY NMR.
MEDLINE=98013176; PubMed=9353127;
Luh F.Y., Archer S.J., Domaille P.J.,
Brotherton D.H., Raine A.R., Xu X., I
Laue E.D.;
"Structure of the cyclin dependent k:
Nature 389:999-1003(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL KAPLAN;
MEDLINE-95257948; PubMed=7739547;
Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.
"Novel INK4 proteins, p19 and p18, are specific inhibitors
cyclin D-dependent kinases CDK4 and CDK6.";
Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                            Chan F.K.M., Zhang J., Cheng L., Shapiro "Identification of human and mouse pi9, a inhibitor with homology to pl6ink4."; Mol. Cell. Biol. 15:2682-2688(1995).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Cyclin-dependent kinase 4 inhibitor D (P19-
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                                                              -!- FUNCTION: INTERACTS
-!- SIMILARITY: BELONGS
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MEDLINE=95257949; PubMed=7739548;
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                                                              STRONGLY WITH CDK4 AND TO THE CDKN2 FAMILY OF
                      ω
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                      ANK REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 259; DB 1
Pred. No. 4e-18;
8; Mismatches
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ANK
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                                                                                                                                                                     р.J.,
к., в
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2FACD11CF56340DC CRC64;
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                                                                                                                                                                        Brizuela
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(P19-INK4D).
                                                                                                                                                                                          Smith B.O.,
                                                                                                                                                                                                                                                                                                                            a novel CDK4 and
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CYCLIN-DEPENDENT
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                                                                                                                                                                   Brenner S.L.,
                                                                                                                                                                                          Owen
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Createu, 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cyclin-dependent kinase 6 inhibitor (P18-INK6) vinase 4 inhibitor C) (P18-INK4C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell cycle; Anti-oncogene; Repeat; REPEAT 73 102 ANK 1. REPEAT 106 135 ANK 3. REPEAT 138 166 ANK 3. CONFLICT 17 17 A -> 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:105387; Cdkn2d.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 3.
SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                  MEDLINE-95257948; PubMed-7739547;
Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.
"Novel INK4 proteins, Pl9 and pl8, are specific inhibitors
cyclin D-dependent kinases CDK4 and CDK6.";
Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q60772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDN6_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Ú20497; AAA85437.1;
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                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL KAPLAN;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                   -!- SIMILARITY: CONTAINS 5 ANK REPEATS
                                                                                                       -!- SUBUNIT: HETERODIMER OF P18 WITH
-!- SIMILARITY: BELONGS TO THE CDKN2
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                               -!- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
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musculus (Mouse).
"ervota; Metazoa; Chordata;
"-+heria; Rodentia;
                                                                                                                                                           CELL GROWTH AND PROLIFERATION WITH A CORRELATED ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
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                                                                                 INHIBITORS.
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Sciurognathi; Muridae;
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9E74F5C23B7EBCB2 CRC64;
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No. 3.7e-17
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  through
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; Murinae; Mus
                                                                                                                                                                                    DEPENDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 6 inhibitor (P18-INK6)
kinase 4 inhibitor C) (P18-INK4C).
                                                                                                                                                                                                                                                                                                         Guan K., Jenkins C.W., Matera G.A., Xiong Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 2.
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                                                                                                                                                                                                                                                              CDK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDKN2C OR CDKN6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:105388;
                        ABDLINE-98300433, running and ABDLINE-98300433, running and all ships and a second in the human cyclin-dependent kinase "Structure of the gene encoding the human cyclin-dependent kinase inhibitor pl8 and mutational analysis in breast cancer."; inhibitor pl8 and mutational analysis in breast cancer.";
                                                                                                                                                                     TISSUE=Breast;
                                                                                                                                                                                                                                 "Growth suppression by p18, a p16INK4/MTS: CDK6 inhibitor, correlates with wild-type Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95095079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
VARIANT BREAST CANCER PRO-72
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
                                                                                                                                        MEDLINE=98300299;
                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72
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Bioinformatics Institute. There a
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                                                                                                                                          PubMed=9636670;
                                                                                                                                                                                                                                                                                                                                                          PubMed-8001816;
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33 AN
65 AN
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132 AN
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40.3%;
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ANK 2.
ANK 3.
ANK 4.
ANK 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                p16INK4/MTS1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local S
Matches 56
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PROSITE; PS50297; ANK_REP_REGION; 1
Cell cycle; Repeat; ANK repeat; Disc
REPEAT 4 3 ANK 1.
REPEAT 37 65 ANK 2.
REPEAT 69 98 ANK 2.
REPEAT 102 132 ANK 4.
VARIANT 72 72 A --> P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Tumor suppressor INK4: determination of the solutio pl8INK4C and demonstration of the functional signifi pl8INK4C and pl6INK4A.";
Biochemistry 38:2930-2940(1999).
-1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY W CELL GROWTH AND PROLIFERATION WITH A CORRELATED ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
-1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
-1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJINE-98100086; PubMed-9437433; Venkataramani R., Swaminathan K., Marmorstein R.; Venkataramani R., Swaminathan K., Marmorstein R.; "Crystal structure of the CDK4/6 inhibitory protein pl81NK4c insights into ankyrin-like repeat structure/function and tumor-derived pl61NK4 mutations."; Nat. Struct. Biol. 5:74-81(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lapointe J., L
"A pl8 mutant cells.";
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                 Pfam; PF00023; ank; 4
SMART; SM00248; ANK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
MEDLINE-98100086; PubMed-9437433;
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       62
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PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 121
                           EPWGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGAN 62
                                                      *EPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAE
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AF041248; AAC39782.1; -.
AF041250; AAC39783.1; -.
AF041249; AAC39783.1; JOINED
                                                                                                    Similarity
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                                                                                      Conservative
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.L., Ericson K.,
                                                                                                                                                          18127
                                                                                                   30.1%;
40.3%;
                                                                                                                                                                                                                                                        repeat; Disease
                                                                                                                                                          MW;
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                                                                                      22;
                                                                              Score 228.5; I
Pred. No. 3.5e
22; Mismatches
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ANK 3.
ANK 4.
A -> P
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/FTId=VAR_001490.
5D66AFA715186E9A
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                                                                                                                                                                                                                                                                      mutation;
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RESULT 11

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                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The Burner by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reputation and characterization of cDNAs encoding ankyrins reveal a family of alternatively spliced J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ankyrin gene.";
Genomics 10:858-866(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 463-495 FROM N.A.
MEDLINE=92009921; PubMed=1833308;
Tse W.T. Menninger J.C., Yang-Feng T.L.,
Lux S.E., Ward D.C., Forget B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain stem;
MEDLINE=94075409; PubMed-8253844;
Chan W., Kordeli E., Bennett V.;
"440-kD ankyrinB: structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANK2_HUMAN STANDARD; PRT; 3924 AA Q01484; Q01485; 01-APR-1993 (Rel. 25, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin Control of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Attach integral membrane p elements. Also bind to cytoskeletal ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 PRODUCED BY ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EMEuropean Bioinformatics Institute. There are no restably non-profit institutions as long as its content
      X56957;
X56958;
Z26634;
M37123;
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PHOSPHORYLATED AT MULTIPLE
EACH PHOSPHORYLATION EVENT F
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; CAA40278.1;
; CAA40279.2;
; CAB42644.1;
; AAA62828.1;
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Query Match
Best Local Similarity
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InterPro; IPR000488; Death.
InterPro; IPR000906; ZUS.
Pfam; PF00023; ank; 24.
Pfam; PF000531; death; 1.
Pfam; PF00791; ZUS; 1.
Pfam; PF00794; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00248; ANK; 21.
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Q -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
(IN ISOFORM 2).

MISSING (IN ISOFORM 2 AND ISOFORM 3).

GQ -> PE (IN REF. 4).

I -> S (IN REF. 1).
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InterPro; IPR000906; ZU5.
Pfam; PF00023; ank; 23.
Pfam; PF000531; death; 1.
Pfam; PF00791; ZU5; 1.
Pfam; PF00791; ZU5; 1.
PRINTS; PR01415; ANKYRIN.
SMART; SM000248; ANK; 22.
SMART; SM00025; DEATH; 1.
SMART; SM000218; ZU5; 1.
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Q02357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
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-1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL ELEMENYS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, THANK ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO TOTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN. ERYTHROCYTE AKVERINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92345717; PubMed=1386265; White R.A., Birkenmeier C.S., Peters L.L., Barker J "Murine erythrocyte ankyrin cDNA: highly conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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MEDLINE=92345717; P
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PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
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RESULT 13
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YB23_HI
YB23_HI
AC Q9ULJ7
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT Hypoth
GN KIAA12
OS HOMO S
OC EUKARY
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RC TISSÜE
RX MEDLIN
RA Nagase
RA Ohara
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Q9ULJ7;
16-OCT-2001 (1
16-OCT-2001 (1
16-OCT-2001 (1
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                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50017; DEATH_DOMAIN; 1.
                                    SEQUENCE FROM N.A.
                                                                                KIAA1223
       Ohara O.;
              Nagase T., Ishikawa K.-I.,
                      MEDLINE=20039619; PubMed=10574462;
                              TISSEE-Brain
                                                  NCBI_TaxID=9606;
                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                     503
 Prediction
                                                                                                                                                             620 YGGSANAESVQGVTPLHLAAQEGHTEM
                                                                                                                                                                                         563 KNGLT-PLHVAVHHNNLDIVKLLLPRGGS--PHSPAWNGYTPLHIAAKQNQIEVARSLLQ
                                                                                                                                                                          123 --- RAAAGGTRGSNHARIDAAEGPSDI 146
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                                                                                                                                                                                                      PATLTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL--
                                                                                                                                                                                                                    LHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG
                                                                                                                                                                                                                                  LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1387
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
l protein KIAA1223 (Fragment).
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                                                                                                                                                                                                                                                                                                  coding
                                                          Primates;
                                                                 Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat; Phosphorylation; Lipoprotein.
89 KDA DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).
sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN).

55 KDA REGULATORY DOMAIN ()
THE BINDING OF ANKYRIN TO
AND THE BAND 3 PROTEIN).
                Kikuno
                                                                                                                                                                                                                                                Score 137.5; Pred. No. 2.9e
                                                                                                                                                                                                                                                                                     ME.
                                                                                                                                                                                                                                                                                                   ANK
                                                                                                                                                                                                                                                                                           DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KDA DOMAIN (SPECTRIN
                                                         Catarrhini; Hominidae; Homo
                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                          PRT;
                                                                                                                                                             646
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17.
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                Hirosawa
 unidentified
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2.9e-05;
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                Χ.
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                Nomura
  human
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 ANKI_HIMAN
ID ANKI_HI
AC P16157
DT 01-APP
DT 01-APP
DT 01-MAR
DT 01-MAR
ON ANKI
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OC EUkary
OC Manmal
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RN [1]
RN SISUE
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Matches 49
                                                                                              ANK1_HUMAN P16157;
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                                                                                                                                        SNIDQRGYDGRNALRVAALEGHRDI
                                                                                                                                                      -RAAAGGTRGSNHARIDAAEGPSDI 146
                                                                                                                                                                                                                                                                 768
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002110; ANK. Pfam; PF00023; ank; 13. SMART; SM00248; ANK; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete sequences of 100 new cDNA clones fro for large proteins in vitro.";
DNA Res. 6:337-345(1999).
-!- SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB033049; BAA86537.1; -. HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                           Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50088; ANK_REPEAT; 13. PROSITE; PS50297; ANK_REP_REGION;
                                             124 LLAAASMGHASVVNTLLFWGAAVDSIDSEGRTVLSIASAQGNVEVVRTLLDRGLDENHRD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete sequences of 100 new
                                                                   LATAAARGRYEEYRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD
DAGWT-PLHMAAFEGHRLICEALIEQGARTNEIDNDGRIPFILASQEGHYDCVQILLENK
                     PATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL----
                                                                                          49; Conservative
                                                                                                                                                   ΑA;
                                                                                                                                                                         11
44
42
115
118
148
181
214
214
214
214
214
313
313
313
                                                                                                                                                   82819 MW;
                                                                                                    17.6%;
                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                           14;
                                                                                         Score 133.5; DB
Pred. No. 2.6e-05
4; Mismatches 7
                                                                                                                                                                         ANK
                                                                                                                                                   2913B69BE2DFE06D CRC64;
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6.
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11
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                                                                                                                 DB 1;
                                                                                            75;
                                                                                                                Length
                                                                                            Indels
                                                                                                                  768;
                                                                                           7;
                                                                                           Gaps
                        122
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seg
01-MAR-2002 (Rel. 41, Last ann
                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
TISSUE-Hematopoietic, MEDLINE-90158830; Pul
                                                                                                                                                         Ankyrin 1 (Erythrocyte ANK1 OR ANK.
                                     SEQUENCE FROM N.A., PARTIAL SEQUENCE,
                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                   STANDARD;
    PubMed=2137557
                                                                                                                                                                              Last sequence update)
Last annotation update)
e ankyrin) (Ankyrin R).
                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                     1880
                                            AND
                                                                                                                                                                                                                                                                                     AA
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InterPro; IPR002110; ANK.
InterPro; IPR00048; Death.
InterPro; IPR00096; 2U5.
InterPro; IPR00096; 2U5.
InterPro; IPR00093; ank; 23.
InterPro; IPR00021; death; 1.
InterPro; IPR00021; ANKYRIN.
SMART; SM00248; ANK; 22.
SMART; SM00025; DEATH; 1.
SMART; SM00018; ZU5; 1.
SMART; SM000218; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=90175370; PubMed=1689849;
Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P.,
Lambert S., Yu H., Palek J.;
Cheung M.C., Kan Y.W., Palek J.;
"CDNA sequence for human erythrocyte ankyrin.";
"CDNA sequence Sci. U.S.A. 87:1730-1734(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDER S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A., Gallagher P.G., Schroeter W., Forget B.G., Lux S.E., "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis."; lat. Genet. 13:214-218(1996).
                                                                                                                                                                                                                                                                                                                                                                    EMBL; X16609; CAA34610.1; -.

MBL; AAA51732.1; -.

IR; S08275; SJHUK.

PIR; A35049; A35049.

HSSP; C00421; 1AWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lux S.E., John K.M., Bennett V.; "Analygis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
   DOMAIN
                                                                                                        Cytoskeleton;
                                                                                                                          PROSITE;
                                                                                     Phosphorylation; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                         MIM; 182900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: At least 3 isoforms; 2/2.2 and 3; are produced by alternative sperm: REGULATED BY PHOSPHORYLATION.

PTM: ACYLATED BY PALMITIC ACID GROUP(S).
DISEASE: Defects in ANK1 are the cause of dhereditary spherocytosis (HS).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO T CYTOSKELETAL PROTEINS FODRIN, TUBULLIN, VIMENTIN AND DESMIN. BESTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS. SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN GP85, AND TO THE ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN GP85, AND TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins.";
344:36-42(1990).
                                                                                                                   PS50088; ANK_REPEAT; 20.
PS50297; ANK_REP_REGION; 1.
PS50017; DEATH_DOMAIN; 1.
   827
                                                                                    Alternative splicing; Repeat; ANK on; Lipoprotein; Disease mutation;
                                      10
   1381
                                    0
826
89 KDA DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).
62 KDA DOMAIN (SPECTRIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of dominant and recessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s; 1/2.1 (shown splicing.
                                                                                    repeat;
Elliptocytosis;
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В
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Best Local S
Matches 52
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VARSPLIC
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                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                              506
                                   67
                                                          œ
YGGSANAESVQGVTPLHLAAQEGHAEM
                       KNGLT-PLHVAVHHNNLDIVKLLLPRGGS--PHSPAWNGYTPLHIAAKQNQVEVARSLLQ
                                                      LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD
          ---RAAAGGTRGSNHARIDAAEGPSDI
                              PATTTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL--
                                              LHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAAKYGKVRVAELLLERDAHPNAAG
                                                                     Similarity 52; Conserv
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                                                                                                   229
1545
1880
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                                                                      Conservative
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398
431
464
497
530
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                                                                           17.6%;
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                                                                      15;
                                                                                                  A -> S (IN REF. 2).
V -> I (IN REF. 2).
MW; 1C5F5E7EFD1CD428
                                                                    Score 133.5; DB 1
Pred. No. 7.1e-05;
5; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN).

55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
                                                                                                                                                                                                                                         MISSING (IN ISOFORM 2).
H -> D (IN ISOFORM 2).
TVEGPLEDPSELEVDIDYFMKHSKDHTSTPNP
                                                                                                                                                                                                                                                                      /FTId=VAR_000602
R -> D.
                                                                                                                                                                                                                                                           DEATH
                                                                                                                                                                                                                                                                 ANK
                                                                                                                                       D -> N (IN DUESSELDORF).
                                                                                                                                                                                          /FTId=VAR_000596.
R -> H (IN BRUEGGEN).
/FTId=VAR_000597.
                                                                                                                                                                                                                                   GLQPDLIEGRKGAQIVKRASLKRGKQ (IN ISOFORM
                                                                                                                     /FTId=VAR_000603
                                                                                                                                            /FTId=VAR_000600
                                                                                                                                                        /FTId=VAR_000601
                                                                                                                                                                    /FTId=VAR_000599
                                                                                                                                                                                /FTId=VAR_000598
                                                                                                                                                                                                                  /FTId=VAR_000595
                                                                                                                                                                                                             -> I (IN HS)
           146
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                                                                                                                                                               U
                                                                      69;
                                                                      Indels
                                                                                 Length
                                                                                                   CRC64;
                                                                                 1880;
                                                                      11;
                                                                     Gaps
                       622
                                   122
                                                                                                                                                                                                                                          ELRGS
                                              565
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RESULT 15

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PRINTER REPORTED TO THE PRINTER PRINTE
                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00023; ank; 8.

Pfam; PF000531; death; 1.

Pfam; PF00069; pkinase; 1.

SMART; SM00246; ANK; 7.

SMART; SM00246; ANK; 7.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS50038; ANK_REPEAT; 6.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS50017; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
                            Phosphorylation; I
DOMAIN 13
DOMAIN 267
REPEAT 378
REPEAT 411
REPEAT 478
REPEAT 511
REPEAT 511
REPEAT 577
REPEAT 610
REPEAT 610
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InterPro; IPR000488; I
InterPro; IPR000719; I
InterPro; IPR002290; S
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MEDLINE-95129831; PubMed-7828849;
MEDLINE-95129831; PubMed-7828849;
Poliss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
"Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAPK_HUMAN STANDARD; PRT; 1431 AA. P53355; 01-0CT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Death-associated protein kinase 1 (EC 2.7.1.-) (DAP kinase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q63450
MIM; 600831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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se; Serine/threonine-protein Kinase; Calmodulin-binding;
lation; ATP-binding; Repeat; ANK repeat; Apoptosis.

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CALMODULIN-BINDING.
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Ser_thr_pkinase
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                  AGARLDVRDAWGRLPVDLAEELGHRDVARYL
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ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

K->A: LOSS OF ACTIVITY.

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Search completed: September 19, 2002, 17:27:22 Job time: 221 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD
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Q9eq34 mesocricetu
Q9ph0 mesocricetu
Q9r023 rattus norv
P97510 mus musculu
Q8v251 felis sire
O9tsyl sus scrofa
O9xs52 fells silve
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O9gmf2 canls famil
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O9z1c1 mus spretus
O9tsy0 sus scrofa
O54846 mus musculu
O9z1c2 mus spretus
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|-------------------|--------|--------|--------|--------|--------|--------|--------|--------|---------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------|------------|--------------------|--------|--------|--------|--------|--------|
| 134 | 134 | 134.5 | 134.5 | 136 | 137 | 137 | 137 | 137.5 | 137.5 | 138 | 142 | 146 | 146 | 149.5 | 157 | 209 | 231.5 | 234 | 254 | 264.5 | 282 | 290 | 292 | 314.5 | 326 | 326 | 327 | 331 |
| 17.6 | 17.6 | 17.7 | | | 18.0 | 18.0 | 18.0 | 18.1 | 18.1 | 18.2 | 18.7 | 19.2 | 19.2 | 19.7 | 20.7 | 27.5 | 30.5 | 30.8 | 33.4 | 34.8 | 37.1 | 38.2 | 38.4 | | | 42.9 | | 43.6 |
| 1181 | 1181 | 968 | 782 | 42 | 1327 | 300 | 299 | 1848 | 1098 | 1136 | 42 | 1265 | 1166 | 1101 | 843 | 116 | 168 | 58 | 166 | 164 | 124 | 124 | 124 | 112 | 113 | 113 | 113 | 113 |
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| Q9VBP3 | Q9XZ37 | Q9VCM6 | Q9BZL4 | Q9Z1C3 | 095271 | Q9UGV1 | Q91WK7 | Q61302 | Q61304 | Q9N180 | Q9Z1E8 | Q9HAS4 | Q9H2K2 | Q9NXY9 | P97582 | 095440 | Q9D153 | 097886 | Q91YV3 | Q9DES3 | Q9DES6 | 09W6I8 | P70067 | Q9QWH4 | Q9QWH6 | Q9QWH7 | Q9QWH8 | Q9QWH5 |
| Qyvbp3 drosopniia | | _ | | 3 mus | _ | homo | / mus | mus | mus | Sod | Q9zle8 mus spretus | | nomo | | rat | | 3 mus | 097886 equus cabal | Q91yv3 mus musculu | | | | P/006/ xiphophorus | _ | mus | mus | mus | mus |

ALIGNMENTS

RESULT Q9NP05

O9NP05 PRELIMINARY; Q9NP05; 01-OCT-2000 (TrEMBLrel. 15, 01-DCT-2000 (TrEMBLrel. 19,

Created) PRT;

> 106 A

Last sequence update)
Last annotation update)

CDK4I PROTEIN (FRAGMENT). CDK4I.

Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILINE=94203288; PubMed=8152487;

MEDILINE=94203288; PubMed=8152487;

NOBORI T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;

Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;

"Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple
human cancers.";

Nature 368:753-756(1994).

MATURE 368:753-756(1994).

EMBL; S69822; AAD14050.1; ".

EMBL; S69822; AAD14050.1; JOINED.

HSSP; P42771; IBI7.

TELECOTION TERPORATION ANX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANK repeat; Repeat.
NON_TER 1
SEQUENCE 106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_REP_REGION;
         103 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                             43
                                                                                                                                                          VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 1.02
                                                                                              VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AA; 11314 MW;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                72.1%; Score 548; DB 4;
100.0%; Pred. No. 2.3e-39;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                               Length 106;
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RESULT Q9
ID Y9
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Q9EQ33
ID Q9
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EQ33 PRELIMINARY; PRT; 157 AA. Q9EQ33; Q1-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) CYCLIN-DEPENDENT KINASE INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91YF9 PRELIMINARY; PKT; LJV AA. Q91YF9; O1-DEC-2001 (TrEMBLrel. 19, Created) O1-DEC-2001 (TrEMBLrel. 19, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update) P151NK4B CYCLIN-DEPENDENT KINASE INHIBITOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mesocricetus auratus (Golden hamster)
Eukaryota; Metazoa; Chordata; Craniatz
Mammalia; Eutheria; Rodentia; Sciurogr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
Mesocricetus.
ANK repeat; Kinase; Repeat.
SEQUENCE, 157 AA; 16635 MW;
                                                  InterPro; IPR002110; ANK.
SMART; SM00248; ANK; 4.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF292567; AAG44950.1; -. HSSP; P42771; 1BI7.
                                                                                                                                                                                                                 Muscarella P., Knobloch T.J., Weghorst C.M.;
"Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene
Identification of Inactivating Alterations in Hamster Tur
Lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Homozygous Deletion of p151NK4b/p161NKa Gene Locus in : Hamster Tumor Cell Lines.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; AJ302037; CAC67498.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10036;
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                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
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Rodentia;
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85.0%;
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Pred. No. 3.3e-36;
4; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Cricetinae;
     06FD66AE6B30DCF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4C04DD3F8C6FF013 CRC64;
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RESULT
Q9ROZ3
ID Q0
AC Q0
DT 00
DT 00
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Best Local Similarity
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Q9R0Z3;
Q9R0Z3;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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01.JUN-2001 (TrEMBLrel. 17, Last sequence update)
01.JUN-2001 (TrEMBLrel. 19, Last annotation update)
01.DEC-2001 (TrEMBLRel. 19, Last annotation update)
CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).
Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Fammanlia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002110; ANK.
SMART; SM00248; ANK; 4.
PROSITE; PS50297; ANK_REP_REGION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muscarella P., Knobloch T.J., Weghorst C.M.; "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and Identification of Inactivating Alterations in Hamster Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                      YLRAAGNTPQGSEPAGVTSAQTP
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(TrEMBLrel.) (TrEMBLrel.
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68.9%;
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70.6%;
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Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 501; DB 11;
Pred. No. 3.2e-35;
.5; Mismatches 27;
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Pred. No. 6e-36;
                                                                                                                 PRT;
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RESULT
P97510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GREE
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Best I
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                                                                                                                                                                                                                "Cdkn2a, the p19ARF, is a Pctr1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P97510 PRELIMINARY; PRT; 168 AA.
P97510; P97937;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
07CLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR P36INK4A)
(P16INK4A)
DEPENDENT KINASE INHIBITOR PROTEIN).
CDKN2A OR E1ALPHA OR P16INK4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-DBA/2N; TISSUE-SPLEEN;
MEDLINE-98151529; PubMed-9482902;
MEDLINE-98151529; PubMed-9482902;
Zhang S., Ramsay E.S., Mock B.A.;
"Cdkn2a, the cyclin-dependent kinase inhibitor encoding pl6INK4a pl9ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANK repeat;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                          STRAIN=VARIOUS STRAINS;
MEDLINE=97179476; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L81167; AAD48924.1; HSSP; P42771; 1BI7. InterPro; IPR002110; ANK.
                         "Sequence variation and chromosomal suppressor gene.";
                                                                        Herzog C.R.,
                                                                                                                                            SEQUENCE OF 1-42
                                                                                                                                                                                           Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P16 PROTEIN P16INK4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLRYLLSSAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSNCEDPTTLSRPVHDAAREGFLDTLVVLHQAGARLDVRDAWGRLPLDLALERGHHDVVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MESSADRLARAAALGREHEVRALLEAGASPNAPNTFGRTPIQVMMGNVKVAALLLSYGA
  Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
8:65-66(1997)
                                                                        You M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17:1366-1374(1997).
                                                                                                                                                                                         Sci. U.S.A.
                                                                                               PubMed=9021155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.7%;
74.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 476.5;
Pred. No. 4.2e
ll; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                         95:2429-2434(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3C4CA920A1FEAEB6 CRC64
                                               mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; |
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                             the
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                                               murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159;
                                               Cdkn2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPPRESSOR
(CYCLIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ψ
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DP PA

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DSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVR

120

EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120

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                                                                                                              Matches
                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE OF 1-155 FROM N.A.
STRAIN=C57BL/6J X DBA;
Ac Castro I.
                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                             Gong
                                                                                                                                                                                                                                                                                                                                                                                                                                              [7]
SEQUENCE OF 1-42 FROM N.A.
STRAIN=CAST/EI, C57BL/6J, ARF/J, AND MOI
Santos J., Melendez B., Perez de Castro
Santos J., Mernandez-Piqueras J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-42 FROM N.A. STRAIN=DBA/2, AND C57BL/6; Gressani K.M., Rollins L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; "Cloning and characterization of murine pl6INK4a and pl5INK4b genes."; oncogene 11:635-645(1995).
                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malumbres M., de Castro I., Santos J., Melendez B., Serrano M., Pellicer A., Fernandez-Piqueras J.;
                                                                                                             ANK repeat;
                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SVJ;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pellicer A., Fernandez-Piqueras "Comparative analysis of the pl6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The 5'-flanking region of the El alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-11 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95380169; PubMed=7651726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1997)
                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                    "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-42 FROM
                                                                                                                                                                         nterPro;
                                                                                                                                                fam; PF00023; ank; 4.
MART; SM00248; ANK; 1.
                                                                                                                                                                                                                       ;; U66086; AAB39600.1; JOIN
;; AF004588; AAB61416.1; --
;; U47018; AAC52987.1; --
;; U79628; AAD00226.1; --
;; U79625; AAD00223.1; --
;; U79627; AAD00225.1; --
                                                                                                                                                                      MGI:104738; Cdkn2a.
rPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                             Z., Li J., Fu J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1) gene.";
180:213-215(1996).
          MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
MESAADRLARAAAQGRVHDVRALLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGA
                                                                                                                                                                                                                                                                                                  U66087; AAB39600.1;
                                                                                                                                                                                                                                                                                                            U49280; AAC00052.1;
                                                                                                                                                                                                                                                                                                                            AF044336; AAC08963.1;
                                                                                                                                                                                                 P42771;
                                                                                                                                                                                                             AF332190; AAK83159.1;
                                                . Similarity
99; Conser
                                                                                                                                                                                                                                                                                                                                   and structure analysis of murine p16INK4a."; d(DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                           PS50297; ANK_REP_REGION; 1. at; Cyclin; Kinase; Repeat. 168 AA; 17941 MW; 9A6B0
                                                 Conservative
                                                                                                                                                                                                 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND C57BL/6;
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                                                           62.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                      JOINED.
                                                 16;
                                                                                                                                                                                                                                                                         .'
                                                                                                          Repeat.
V; 9A6B0F24F34D5FEC
                                                           Score 476;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      p16(INK4a) and p15(INK4b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller M.S.;
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND MOLF/EI;
                                                          o
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                                                             5e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form of the murine pl6INK4a
                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malumbres M.,
                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
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                                                                                                              CRC64;
                                                                      Length 168;
                                                 Indels
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                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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O89088;
O1-NOV-1998 (TrembLrel. 08, Created)
O1-NOV-1998 (TrembLrel. 08, Last sequence update)
O1-DEC-2001 (TrembLrel. 19, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR PLOINK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
CDKNNA OR EIALPHA OR P16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-42 FROM N.A.
STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
Santos J., Melendez B., Perez de Castro I., Malumbres M., S
Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA
in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044335; AAC08962.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS50297; ANK_REP_REGION; 1.
ANK repeat; Cyclin; Kinase; Repeat.
SEQUENCE 168 AA; 17915 MW; 356A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/CANPT; TISSUE-SPLEEN;
MEDLINE-98151529; PubMed-9482902;
Zhang S., Ramsay E.S., Mock B.A.;
"Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARR, is a candidate for the plasmacytoma susceptibility locus, Pctrl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-MA/M4J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herzog C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97179476; PubMed=9021155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-42 FROM
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                                                                                                           121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 155
                                                                                                                                                                      DSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVR
                                                                                                                                                                                                    EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                         MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                                                                                                                                                                                       MESAADRLARAAAQGRVPDVRALLEAGVSPNAPNSFGRTPIQVMMMGNVHIAALLLNYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U49279; AAC00051.1; -.
U79626; AAD00224.1; -.
P42771; 1BI7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          You M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           62.4%;
63.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Score 474; DB 11;
Pred. No. 7.3e-33;
7; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356A973BEAC4D167 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 168;
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RESULT
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Best Local
ANK repeat;
NON_TER
NON_TER
                                                                                                                                                                                                                                                               Q9TSY1;
Q9TSY1;
01-MAY-2000
                                                                   Submitted (JUN-1999)
EMBL; AJ242787; CAB6!
HSSP; P42771; 1BI7.
                                Pfam; PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                   sequences."
                                                                                                                                    STRAIN=LARGE WHITE;
                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.; "Cloning and chromosomal mapping of the feline genes pl6(MTS1/CDKN2A) and pl5(MTS2/CDKN2B)."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                        InterPro; IPR002110; ANK.
                                                                                                             Le Chalony C., Hayes H., Fre "Identification and mapping
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                    CDKN2A
                                                                                                                                                                                                                                CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9XS51;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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NON_TER 1
NON_TER 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; pr00023; ank; 3.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PERIPHERAL BLOOD;
Okuda M., Cho K., Setogu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002110; ANK.
                       Kinase; Repeat.
                                                                                                                                                                                                                         (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
(TremBLrel. 19, Last annotation updat
NDENT KINASE INHIBITOR, P16 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AA;
  103
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                                                                              1999) to the CAB65454.1;
  103
                                                                                                                                                                                Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               59.1%;
86.0%;
                                                                                                               H., Frelat G., (
napping of swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
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                                                                                          EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 449; DB 6;
Pred. No. 5.5e-31;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26399FF21359F35D CRC64;
                                                                                                                          Geffrotin
                                                                                                               GDKN2A and CDKN2B exon2
                                                                                                                                                                                                                                                                                      103
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                                                                                                                                                                                                                             tion update) (FRAGMENT).
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on update)
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                                                                                                                                                                                              Euteleostomi;
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SQ

SEQUENCE

103 AA;

11023 MW;

5D23ABCC1088DE0B CRC64;

Length 103

Match

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RESULT
Q9XS52
ID Q9
RESULT
Q9GMF2
ID Q9G
AC Q9G
DT 01
DT 01
DT 01
DT 02
CY
OS CC
OS CC
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RP SE
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Best Loc
Matches
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                                      Q9GMF2
Q9GMF2;
Q19GMF2;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
Canis familiaris (Dog).
Cunis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PERIPHERAL BLOOD;
Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M.,
Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
"Cloning and chromosomal mapping of the feline genes pl6
and p15(MTS2/CDKN2B).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB018089; BAA33541.1; -.
HSSP; P42771; 1B17.
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XS52 PRELIMINARY; PRT; 86 AA. Q9XS52; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) P15/MTS2/CDKN2B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  ANK repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00023; ank; 2
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9685;
 SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VMMMGSTRVAELLLLHGADPNCEDPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 60
                                                                                                                                                                                                                                                        GRLPVDLAEELGHRDVARYLRAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRLPVDLAEERGHRDVAGYLRANAGRTEGGSHARSNSGEDPA 102
                                                                                                                                                                                                                                                                                      VMMMGSARVAELLLLHGADPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW
                                                                                                                                                                                                                                                                                                     VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW
                                                                                                                                                                                                                               GRLPVDLAEERGHRDVARYLRAAAG
                                                                                                                                                                                                                                                                                                                                              83;
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                                                                                                                                                                                                                                                                                                                                                          56.2%;
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                                                                                                                                                                                                                                                                                                                                           Score 427; DB 6;
Pred. No. 3.3e-29;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                    A59FF0193290E867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
; Fissipedia; Felidae;
                                                                                                                                                                                                                                                            127
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.5e-30;
                                                                                                                                                                                                                                                                                                                                                                        Length 86
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Felis.
                                          Euteleostomi; Canis.
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RESULT

13

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Вb
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Best Local
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Best Local
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pellicer A., Fernandez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79639; AAD00234.1; -.
EMBL; U79638; AAD00233.1; -.
EMBL; U79638; AAD00233.1; -.
EMBL; U79638; AAD00233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QUPO
Q9QUPO;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANK repeat; Kinase; Repeat.
NON_TER 1 1
NON_TER 81 81
SEQUENCE 81 AA; 8868 MW;
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"Role of p16/Ink4-a in familial canine cancers.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF234176; AAG01087.1; -.
HSSP; P42771; 1B17.
InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                  ANK repeat; Cyclin; Kinase;
NON_TER 1 1
NON_TER 86 86
SEQUENCE 86 AA; 9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_REP_REGION; 1.
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                                               103
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61
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                                                                                         GRLPVDLAEELGHRDVARYL
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GRLPVDLAEEQGHRDIARYLHAATG
                       GRLPVDLAEELGHRDVARYLRAAAG
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79; Conserv
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Rodentia;
                                                                                                                                                                                                                    53.7%;
92.9%;
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                                                                                                                                                                                            Score 408;
Pred. No. 1.
2; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 409; DB 6; Pred. No. 1e-27;
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                                                                                                                                                                                                                                                                                                                     509D9B3613251B18
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                                            127
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                                                                                                                                                                                                                      .4e-27;
                                                                                                                                                                                                                                              DB 11;
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Q9Z1C1
AC Q9Z1C1;
DP 01-MAY-1
DT 01-MAY-1
DT 01-DEC--
DE CYCLIN-4
GN P15(INK-4
GN P15(INK-4
GN MUS SPIE
OC EUKARYOT
OC MAMIMALIA
OX NCBL_TAB
RN [1]
RN [1]
RR SEQUENCE
RA SENTOS :
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Best Local S
Matches 79
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O9TSYO;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGME)
P15(INK4B)
                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-LARGE WHITE;

MEDLINE-20290998; PubMed-10828598;

Le Chalony C., Hayes H., Frelat G., Geffrotin C.;

"Identification and mapping of swine cyclin-dependent kinase inhibitor CDKN2A and CDKN2B exon2 sequences.";

Cytogenet. Cell Genet. 88:240-243(2000).

EMBL; AJ242788; CAB65455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pellicer A., Fernandez-Piqueras J.; "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains."; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U79637; AADD00237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus spretus (Western wild mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDKN2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANK repeat; Kinase; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Santos J., Melendez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRET/EI;
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                                ANK repeat; Kinase; Repeat.
                                                                                                           InterPro; IPR002110; ANK. Pfam; PF00023; ank; 2.
                                                                                                                                                               HSSP; P42771;
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002110; ANK.
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SEQUENCE
                                                                                Pfam; PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 GRLPVDLAEELGHRDVARYLRAAAG
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          86
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6 AA;
          A,
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9269 MW;
          9286
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Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B., Perez de Castro
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92.9%;
          MW;
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Pred No. 1
        16EF7A223293CCF9 CRC64;
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.4e-27;
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(FRAGMENT).
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Sus.
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RESULT
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AC O54
AC O54
DT O11
DT O11
DT O11
DT O1
OS M
OC E E
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Best Local Similarity
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Best Local
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01-JUN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANK repeat; Kinase; Repeat.
NON_TER 1 1
SEQUENCE 86 AA; 9237 MW;
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EMBL; AF015460; AAB94534.1; -.
HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99124385; PubMed=9927195; Malumbres M., de Castro I.F., Santos J., Piqueras J.F., Pellicer A.; Malumbres M., de Castro I.F., Santos J., Piqueras J.F., Pellicer A.; "Hypermethylation of the cell cycle inhibitor p151NK4b 3'-untranslated region interferes with its transcriptional regulation in primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-C57BL/6J;
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PROSITE; PS50297; ANK_REP_REGION;
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Mammalia; Eutheria;
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3; Mismatches 3
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Human W9 protein s Antiproliferative Angiogenesis inhib Truncated p27/p16

Human W9 protein s Antiproliferative Angiogenesis inhib Truncated p27/p16

AAW10627 AAW74549 AAW40524 AAW80524 AAW80529 AAW97524 AAY97524 AAY96067 AAY96067 AAY91102 AAY59415

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ALIGNMENTS

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| WPI; 1995-344626/44. | Cannon-Albright LA, Kamb A, Skolnick MH; | (UTAH) UNIV UTAH RES FOUND. | (MYRI-) MYRIAD GENETICS INC. | | | 18-MAR-1994; 94US-0215087. | | 18-MAR-1994; 94US-0214582. | | | 17-MAR-1995. 95W0-11503537 | 1000 | 28-SED-1995. | | WO9525813-A1. | | Homo sapiens. | | pancreas; breast; thyroid. | <pre>predisposition; melanoma; leukaemia; lymphoma; prognosis;</pre> | Multiple tumour suppressor; MTS1; cancer; diagnosis; assay; | | Multiple tumour suppressor 1 (MTS1) polypeptide. | | 08-MAY-1996 (first entry) | | AAR81701; | | AAR81701 standard; Protein; 148 AA. | 1701 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS1 gene ORF ART00736 (which encodes AAR81701) mutant sequences AAT00749/50. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                     94US-0251938.
94US-0214581.
94US-0214582.
94US-0215088.
94US-0227369.
94US-0215086.
94US-0215087.
                                                                                                                                         GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour suppressor polypeptide, MTS1.
                                                                                                                                                                                                                                                                                                                                                                                           95WO-US03316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 760; DB 16;
Pred. No. 6.6e-83;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glioma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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AAR53401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
Detection of subunit components of cyclin complexes diagnosing transformation of a cell and developing \boldsymbol{j}
                                            WPI; 1994-151320/18
N-PSDB; AAQ63491.
                                                                                                                                                                                                                                                                                   Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia; lymphoma; cell cycle; detection; identification; tumour virus; proliferating cell nuclear antigen; subunit; complex.
                                                                                                                                        16-OCT-1992;
17-DEC-1992;
                                                                                     Beach DH,
                                                                                                                                                                                                           28-APR-1994
                                                                                                                                                                                                                                      W09409135-A
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTS polypeptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer
                                                                                                              (COLD-) COLD
                                                                                                                                                                                 18-OCT-1993;
                                                                                                                                                                                                                                                                                                                                              Inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR53401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence is the MTS polypeptide MT MTS polypeptide encoding cDNAs and mutants of these are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild-type multiple tumour suppressor - useful in diagnosis, prognosis and melanoma or leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt mepsadwlataaar} grveev ralle avalpnapn sygrrpiq vmmmgsarvaell 11 hga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148;
                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 92-93; 156pp;
                                                                                  Xiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                           cyclin dependent kinase 4 (p16INK4).
                                                                                                              SPRING
                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                        92US-0963308
92US-0991997
                                                                                                                                                                                93WO-US09945
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 760; DB 16;
Pred. No. 6.6e-83;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MTS) gene and mutant sequences therapy of human cancer, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148;
              for
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inhibitors

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC in some B-cell lymphomas and leukaemias. D-type cyclin, cyclin CC dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many CC combinatorial variations of the components e.g. cyclin D1 or D3 and CC CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may CC chave a subtly diferent role in the cell cycle or in different cell CC types. Cellular transformation by DNA tumour viruses such as SV40 CC is associated with selective subunit rearrangement of the cyclin D CC complexes. In virally transformed cells, CDK4 totally dissociates CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton CC inhibits CDK4. p161NK4 was discovered to show many similarities to p16. Reagents, such as monoclonal antibodies, can be developed that recognise the interactions between the CDK's cyclins, PCNA and low molecular weight polypeptides and can therefore be used to identify CK
В
                                                                                                                                                                                                                                                                                                                                             Ϋ́
                                                                                                                                                                                                                                                                                                                                                                    AAR85116
                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                29-NOV-1994;
14-APR-1994;
25-MAY-1994;
14-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 40; 45pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activators, partic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The cell cycle gene implicated most strongly in oncogenesis is the human cyclin D1. It is genetically linked to the bcl-1 oncogene, a locus activated by translocation to an immunoglobulin gene enhancer
                                                                                                                                                                                                                                                                                                                                                       AAR85116 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                               Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor; CCR; cancer; cell proliferation.
                                                                                                                                                                                                                                                                       Cell-cycle regulatory protein
                                                                                                                                                                                                                                                                                                   01-MAR-1996
                                                                                                                                                                                                                                                                                                                             AAR85116;
                                                                                                                                                 26-OCT-1995
                                                                                                                                                                           WO9528483-A1
Beach DH,
                                                                                                                      14-APR-1995;
                        (COLD-) COLD
                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ylraaaggtrgsnharidaaegpsdipd 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA;
Demetrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                  (first
                         SPRING HARBOR LAB.
                                                  94US-0346147.
94US-0227371.
94US-0248812.
94US-0306511.
                                                                                                                        95WO-US04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for cancer treatment
                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
Hannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 760; DB 15; Pred. No. 6.8e-83;
                                                                                                                                                                                                                                                                        p16
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GJ,
Serrano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT
AAY24741
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 Вþ
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Best Local Similarity
Matches 148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was obtd. by expression of a cDNA clone (AAR02962) isolated in a 2-hybrid screening assay. CCR p16 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative
                                                                           18-NOV-1993;
14-APR-1994;
25-MAY-1994;
14-SEP-1994;
29-NOV-1994;
30-JUN-1995;
02-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                         (COLD-)
WPI; 1999-394656/33
                                                                                                                                                        04-APR-1996;
                                                                                                                                                                             04-APR-1996;
                                                                                                                                                                                                06-JUL-1999
                                                                                                                                                                                                                                                                  INK-4; p16; p15; |
transgenic mouse;
                                                                                                                                                                                                                                                                                                 Human INK-4 protein pl6.
                                                                                                                                                                                                                                                                                                                                                                   AAY24741 standard; Protein;
                       Beach DH,
                                                                                                                                                                                                                         US5919997-A
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                        23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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DB; AAT02962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar}
                                           COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 76-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156
                     DePinho RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                 p15; p18; p19; CDK4; cell cycle regulatory protein;
mouse; p16-INK4-a; carcinogen; anti-proliferative.
                                           SPRING H
                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                           96US-0627610

93US-0154915.

94US-0227371.

94US-0248812.

94US-0306511.

94US-0346147.

95US-0497214.

96US-0581918.
                                                                                                                                                                               96US-0627610
                                             HARBOR LAB
                        Serrano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                     156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 760; DB 16;
Pred. No. 7.1e-83;
0; Mismatches 0;
                                              COLLEGE
                        X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT
AAY88354
ID AAY8
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AC AAY8
AC AAY8
XX
DT 14-J
XX
DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                          17-DEC-1992;
18-NOV-1993;
14-APR-1994;
25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a transgenic mouse having germline and sommatic cells which comprise an incorporated transgene that disrupts and inhibits the p16-INK4-a gene leading to tumour susceptibility. Also described is a method of making a mouse and mouse embryonic stem cells a functionally disrupted p16-INK4-a gene which comprises transferring a transgene construct into embryonic stem cells of a mouse and transferring these into a mouse blastocyst and implanting the resulting chimeric blastocyst into a female mouse selecting offspring having an endogenous p16-INK4-a gene allele. The transgenic mouse is useful for evaluating the carcinogenic potential or the anti-proliferative activity of a test compound. The present sequence represents the human INK4 protein p16 given in the present invention.
                                                                                                                                                                                                                                                                                        Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection; cell proliferation; differentiation; neoplasia; cancer; cell growth; cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
           Beach DH, Demetrick
                                                                                                                                                                               02-JAN-1996;
                                                                                                                                                                                                           28-MAR-2000
                                                                                                                                                                                                                                    US6043030-A
                                                                                                                                                                                                                                                                                                                                                  Human cell
                                                                                                                                                                                                                                                                                                                                                                              14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                        AAY88354;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY88354 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic mice with modified cell-cycle regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX80472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ylraaaggtrgsnharidaaegpsdipd 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mepsadwlataaargrveevralleavalpnapnsygrrpiqvmmmgsarvaellllhga
                                         COLD
                                                                                                                                                                                                                                                                                                                                                cycle
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                       SPRING
                                                                            93US-0154915.
94US-0227371.
94US-0248812.
94US-0306511.
94US-0346147.
                                                                   95US-0497214.
                                                                                                                                                   9208-0991997.
                                                                                                                                                                              96US-0581918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45-46;
                                       HARBOR LAB
             DJ,
             Serrano M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                protein p16 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 760; DB 20;
Pred. No. 7.1e-83;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
             Hannon
             GJ;
                                                                                                                                                                                                                                                                                                                                               acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT
AAW23534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC pl6 amino acid sequence. The pl6 gene is located on chromosome 9p11-22.

CT he invention relates to a diagnostic assay which comprises detecting a cc mutation in the pl6 gene, which is used to identify a cell or cells at crisk of developing a disorder characterised by unwanted cell or cells at cc proliferation or differentiation. Pl6 is a cyclin-dependent kinase cc (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle progression and ultimately cell growth. The assay can be used for cell or cells at risk for a disorder (neoplasia) cc diaracterized by unwanted cell proliferation or differentiation. The cc method is used for detecting mutations in either a CCR gene or CDK gene cc which alter complex formation between these two proteins. The method is used for detecting mutations in other cellular proteins which cd is used for detecting mutations in other cellular proteins which cl calso used for detecting mutations in other cellular proteins which disrupt binding of complex formation between these two proteins which complex for detecting mutations in other cellular proteins which disrupt binding of complex of signal transduction proteins such as mass protein or other cellular proteins which interact with ras, e.g. will stumour complex formation in the proteins which are unable to physically interact with a convenient for detecting mutants of CCR genes encoding proteins which are unable to physically interact with a convenient for detecting mutants of CCR what convenient for detecting mutants of CCR what convenient for detecting mutants of CCR genes encoding proteins which are unable to physically interact with a convenient for detecting mutants of CCR genes encoding proteins which are unable to physically interact with a convenient for detecting mutants of CCR what convenient for detecting mutants of CCR what convenient for detecting mutants of CCR genes encoding proteins which are unable to physically interact with a convenient for detecting mutants of CCR genes encoding the detecting mutants 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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N-PSDB;
                                                                                                                                                                       Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene; chimeric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory protein) in a diagnostic assay for identifying a cell at risk for a discrete characterized by unwanted cell proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Column 57-58; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation
                                            Misc-difference
                                                                                                                                                     tissue degeneration;
                                                                                                                                                                                                                                                                  CDK inhibitory fusion
                                                                                                                                                                                                                                                                                                              16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                           AAW23534;
                                                                                                                                                                                                                                                                                                                                                                                                  AAW23534 standard; Protein; 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDK bait protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                             sapiens
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DB; AAA13096.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                              (first entry)
/note= "poly-His tag" 205..219
                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                         therapy
                                                                                                                                                                                                                                                                  protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 7.1e-83;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156
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Misc-difference

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AAW95094
ID AAW9
XX
AC AAW9
XX
DT 25-1
XX
DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculitis, and to inhibit spermatogenesis or ogenesis. The chimeric proteins can also be used in vitro to maintain cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDX/cyclin complex than binding motifs used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CI binding motifs from at least two different proteins that bind to CDKs. The protein controls proliferation and/or differentiation of cells, particularly they inhibit cell-cycle progression. They can be used to treat a wide range of proliferative disorders, e.g. cancer, leukaemia, psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric inhibitor of
therapy of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-393685/36.
N-PSDB; AAT74051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human {\it p27} and {\it p16} cDNA sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 40; Page 38-40; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beach D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1996;
Human p27-p16 fusion protein
                                     25-MAY-1999
                                                                       AAW95094;
                                                                                                           AAW95094 standard; Protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  individually (since they may bind to CDK involved in different stages of
                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                          304
                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 148; Conser
                                                                                                                                                                                                                                                                                                                                                                 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell cycle).
                                                                                                                                                                                                                                                                        epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar
                                                                                                                                                                                                                                                                                                                                            mepsadwlataaargrveevralleavalpnapnsygrrpiqvmnmgsarvaellllhga 303
                                                                                                                                                                                                ylraaaggtrgsnharidaaegpsdipd
                                                                                                                                                                                                                                    YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                            EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0589981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "(Gly4Ser)2 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclin dependent kinase - useful for gene other proliferative and differentiative
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 760; DB 18;
Pred. No. 2.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase (CDK)
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                            363
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1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60

Matches

Local Similarity

Conservative

100.0%; Score 760; DB 20; 100.0%; Pred. No. 2.4e-82; ive 0; Mismatches 0;

Indels

0,

Gaps

0

Sequence

391 AA;

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C(CDKS), particularly CDK/cyclin complexes. It provides a recombinant CC transfection system (A) that comprises: (1) first gene construct CC comprising a sequence encoding an inhibitory polypeptide containing at CC least one CDK. binding motif for binding and inhibiting activity of a CDK.

CC linked to a transcription regulator functional in eukaryotic cells; (1) CC second gene construct comprising a sequence encoding a polypeptide that CC promotes encoding a fusion protein, and (ii) a gene delivery composition for CC delivering the GCs to a cell for transfection. Also provided are nucleic CC polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP CC consists of at least one CDK-binding motif and a TCP. (A) are used to CC treat vascular wounds that involve a break in the endothelium and CC excessive proliferation of smooth muscle, particularly restenosis but CC more generally any repair of cardiovascular damage, arteriosclerotic Lesions or for endothelialisation of synthetic vascular grafts. More CC wide range of situations, e.g. for treating vascular diseases as above; tumours (gliomas, leukaemias); chronic inflammation; neurodegeneration; cc acne; also to control hair growth (e.g. to prevent hair loss caused by chemotherapy or radiation); periodontal disease; to treat tachycardia; ct oinhibit spermatogenesis etc. Chimaeric proteins bind to CDKs so inhibit cell CC cycle progression articularly smooth muscle cell nordiferation made a cell profiferation made cell profiferation articularly smooth muscle cell nordiferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcyclosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 63; Page 70-72; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-153770/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                     cycle progression, particularly smooth muscle cell proliferation. The gene constructs may also be used to produce FP in cell cultures, for production or for regulating cell differentiation in vitro. The pressequence represents a human p27-p16 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel inhibitors of cyclin-dependent kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1997;
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RESULT
AAY97526
ID AAY9
XX
AC AAY9
XX
DT 15-J
XX
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Best Local
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08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CELL-)
                                                                                                                                                                     The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays synchronise cell growth in cultured cells.
                                                                                                                                                                                                                                                                                                                         Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclin dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200052184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; W3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human W3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY97526 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                        This sequence represents the human W3 protein.
                                                                                                                                                                                                                                                                                                Example 1; Page 108-109; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Patel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
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                                    244
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             61
                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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DB; AAA90923.
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           EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                    mepsadwlataaargrveevralleavalpnapnsygrrpiqvmmmgsarvaellllhga
                                              MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLLHGA
148;
                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL GENESYS
                                                                                                                                                                                                                                                                                                                                                                                                             McArthur J,
                                                                                                                                                391 AA;
                                                                                  100.0%; ilarity 100.0%; Conservative
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99US-0128271.
99US-0128515.
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                                                                                                                                                                                                                                                                                                                                                                                                             Gyuris
                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391
                                                                                              Score 760; DB 21;
Pred. No. 2.4e-82;
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                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Mendez
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                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                               Finer
                                                                                     Indels
                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                             391;
                                                                                    0;
                                                                                    Gaps
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RESULT
AAY96041
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                                                                                                                                                                                                                                                                                                                                                   01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                      The present sequence is that of p27-p16 fusion protein W3 comprising an N-terminal 6His tay, the human p27 protein (see AAY96052), a (G1y4Ser)3 hinge and the human p16 protein (see AAY96053). It is encoded by a nucleic acid obtained by PCR amplification of p27 and p16 DNAs using primers that also included codons for the tag/hinge regions. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a
                                                                                                                                                                                                                                                                                                                (CELL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96041;
                                                                                                                                                                                                        Novel recombinant lentivirus for inhibiting proliferation of smooth muscle cells in e.g. restenosis, is replication deficient and compra transgene encoding a cyclin dependent kinase inhibitor \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Syntheti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; p27; p16; human; smooth muscle cell; hyperproliferation; res vasotropic; antiproliferative; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2000
                                                                                                                                                                                                                                                                  WPI; 2000-594183/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY96041 standard; Protein;
                                                                                                                                                                                    Example 1; Page 101-103; 126pp; English
                                                                                                                                                                                                                                                        N-PSDB; AAA50488
                                                                                                                                                                                                                                                                                          Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiproliferative p27-p16 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304
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                                                                                                                                                                                                                                                                                                                 CELL GENESYS INC MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C
                                                                                                                                                                                                                                                                                          Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US04971
                                                                                                                                                                                                                                                                                                                                                   99US-0122974.
99US-0163682.
99US-0457568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= p27
205..219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= 6His_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .391
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                                                                                                                                                                                                                                                                                           Finer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restenosis;
                                                                                                                                                               comprising
                                                                                                                                                                                                               and comprises
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replication-deficient recombinant adenovirus that lacks functional E1 and E4 regions, and comprises a transgene encoding a cyclin dependent kinase inhibitor (CDKi). The CDKi is selected from an INK4 family protein such as human p16, a CIP/KIP family protein such as p27, active fragments of these, or fusion proteins comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein see Aay96046 and AAY96049). The method is to inhibit mammalian smooth muscle cell hyperproliferation, induced

The method is used

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Best Local
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                                                                                              01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by injury caused by angioplasty, stent placement or vein engraftment. It is useful for treating vascular pathologies e.g., restenosis. Also claimed are recombinant lentiviruses encoding
                                                                                                                                                                                                                                                                                                                                   Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; INK4; p27; p1 human; anglogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-2000
 Inhibiting anglogenesis
                                                Patel S,
                                                                 (CELL-) CELL GENESYS (MITO-) MITOTIX INC.
                                                                                                                                      28-FEB-2000; 2000WO-US04970
                                                                                                                                                                            WO200052158-A1
                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                          antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitor (p27-p16 fusion) W3
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96068 standard;
                   N-PSDB; AAA50523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           364
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                                                                                                                                                                                                                         eptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ylraaaggtrgsnharidaaegpsdipd 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148;
                             2000-565501/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                               Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                              99US-0122974.
99US-0163682.
99US-0457646.
                                                                                                                                                                                                                         /label= p27
205..219
                                                                                                                                                                                                         239..391
                                                                                                                                                                                                                                                      /label= 6His_tag
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                               /label= p16
                                                                                                                                                                                                                 /label= Hinge
                                                                                                                                                                                                                                                                                                                          gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 760; DB 21; 100.0%; Pred. No. 2.4e-82; +ive- 0; Mismatches 0;
                                                                             INC
                                                Gyuris
 and treating angiogenesis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 391;
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(TEXA) UNIV TEXAS SYSTEM

17-JUL-1995;

95us-0502881 96WO-US11787 06-FEB-1997 WO9703635-A2 Homo sapiens

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RESULT 12
AAW10627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC comprising an N-terminal fills tag, the human p27 protein (see CC AAY96065), a (Gly4Ser)3 hinge, and the human p27 protein (see CC AAY96067). The fusion protein is encoded by a nucleic acid (see CC AAX96067). The fusion protein is encoded by a nucleic acid (see CC AAX96523) that was obtained by PCR amplification of human p27 and p16 CC DNAs using primers that also included codons encoding the tag/hinge CC angiogenesis involves transducing an epithelial cell with a CC transgene encoding a cell dependent kinase inhibitor (CDK1). The CC transgene encoding a cell dependent kinase inhibitor (CDK1). The CC transgene encoding a protein of the CIP/KIP family such as p27, a CC protein of the INK4 family such as p16, active fragments of these proteins, or a fusion of 2 CDK1 proteins such as p27 and p16. The CC method is useful in treating conditions associated with angiogenesis, CC such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy (claimed). Alternatively, the transgene CC is delivered to an auxiliary cell, and is expressed by that cell current that the CDK1 is released into the blood and contacts the CC CCK4/CyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local s
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin dependent kinase inhibitor \,\cdot\,
                                                                                                                                                                                                                    Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; Cleancer cell; lung cancer; bladder cancer; melanoma; restenosis; anti-angiogenic activity; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 108-110; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                AAW10627 standard; Protein; 156
                                                                                                                                                                                                                                                                                                 Tumour suppressor
                                                                                                                                                                                                                                                                                                                                         28-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%;
Local Similarity 100.0%;
hes 148; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is that of p27-p16 fusion protein prising an N-terminal 6His tag, the human p27 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLFVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 AA;
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                   p16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 760; DB 21;
Pred. No. 2.4e-82;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                   CDK4;
                                                                                                                                                                                                                                                 therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the tumour suppressor p16. The DNA encoding CC this sequence is joined to a promoter functional in eukaryotic cells and cused in the expression construct of the invention. p16 is an inhibitory CC subunit, which is involved in the control of cyclin-dependent kinase 4 cC activity, and functions as a tumour suppressor. By detecting this CC sequence or the DNA encoding it, cancer cells can be detected. When the construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the CC expression construct inhibits p16 function. Reduced or increased levels CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.3
 07-JUN-1995;
18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                               9251
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                                                                                                                                                 Homo
                                                                   18-MAR-1994;
                                                                                            29-APR-1997
                                                                                                                       US5624819-A
                                                                                                                                                                         Human; multiple;
                                                                                                                                                                                                   Human multiple
                                                                                                                                                                                                                                                       AAW19251;
                                                                                                                                                                                                                                                                             AAW19251 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1b;
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                                                                                                                                                                                                                                                                                                                                                        YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                         EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                                                                                                                                                                                                                                            ylraaaggtrgsnharidaaegpsdipd 156
                                                                                                                                                                                                                                                                                                                                                                                              \tt epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar
                                                                                                                                                                                                                                                                                                                                                                                                                                                mepsadwlataaargrveevralleagalpnapnsygrrpiqvmmmgsarvaellllhga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA;
                                                                                                                                                                                                                           (first
95US-0474177.
94US-0214582.
94US-0215086.
94US-0215087.
                                                                                                                                                                                                tumour suppressor 1 gene product
                                                                 94US-0214582
                                                                                                                                                                      tumour; suppressor; MTS1; cancer; diagnosis.
                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92pp; English.
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to transformed
                                                                                                                                                                                                                                                                              156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 753; DB 18;
Pred. No. 4.9e-82;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour suppressor cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
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treating
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RESULT 1
AAW74549
ID AAW7
XX AAW7
XX AAW1
AC AAW7
XX AMIN
XX Mult
KW Mult
KW Soma
XX Soma
XX US58
XX US58
PF 07-J
PR 18-y
PR 1
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Best Local
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                                                                                                    18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                   07-JUN-1995;
                                                             (MYRI-)
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                                                                                                                                                                                                                                                                                                                    01-SEP-1998
                                                                                                                                                                                                                                                                                                                                                           US5801236-A
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          somatic mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of multiple tumour suppressor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW74549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human mutant multiple tumour suppressor gene sequences production of recombinant mutant polypeptide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present (MTS1) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Columns 61-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-258217/23.
N-PSDB; AAT72311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MYRI-)
(UTAH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cannon-Albright LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ylraaaggtrgsnharidaaegpsdipd 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147;
                                                               MYRIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 99.:
47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYRIAD GENETICS INC.
UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product,
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                                                                                                  95US-0480810.
94US-0214582.
94US-0215086.
94US-0215087.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
                                                             GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0227369.
94US-0251938.
95WO-US03537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy
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useful in
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99.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72pp;
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Pred. No. 4.9e-82;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple tumour : cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                       18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to creen for drugs to be used for cancer therapy, and the protein litself may also be used to restore MTS function in a cell.
                                                                                                                                                                            18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                   US5739027-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW40524 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the multiple tumour suppressor 1 (MTS-1) protein, used in the method of the invention. The MTS gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
(MYRI-) MYRIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTS1; multiple tumour suppressor; diagnosis; cancer; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MTS1 protein
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N-PSDB; AAV53819.
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||||||||||||||||||||||||||||
129 Ylraaaggtrgsnharidaaegpsdipd 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 AA;
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                                                 95US-0487033.
94US-0214582.
94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
GENETICS INC
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99.3%;
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Pred. No. 4.9e-82;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          germ-line mutation;
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d to MTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a human multiple tumour suppression protein, MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA specific for Multiple Tumour Suppressor useful for the diagnosis of cancers related mutation(s) and their treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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N-PSDB; AAV11238.
    129
                                                                            121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 4.9e-82;
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to MTS1E1-beta
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Maximum Match 100%
Listing first 45 summaries
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         number of hits satisfying chosen parameters:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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length: 2000000000
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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| ALIGNMENTS | US-08-346-147B-8 | US-08-581-918A-8 | US-08-627-610-8 | US-09-120-131-14 | US-09-201-139-14 | us-09-120-129-14 | US-09-120-128-14 | US-08-986-515-14 | US-09-115-252-14 | US-09-120-130-14 | US-08-486-047-14 | US-08-848-251-14 | US-08-508-735-14 | US-08-480-810-14 | US-08-487-033-14 | US-08-474-177-14 | US-08-346-147B-12 | US-08-581-918A-12 |
| | Sequence 8, Appli | Sequence 8, Appli | Sequence 8, Appli | Sequence 14, Appl | ` | • | Sequence 14, Appl | ` | ` | ` | ` | ` | Sequence 12, Appl |

RESULT 1 US-08-154-915-4

Sequence 4, Application US/08154915 Patent No. 5618669 COFFWARE: ASCII(text) CURRENT APPLICATION UNBER: US/08/154,915 APPLICATION NUMBER: US/08/154,915 FILING DATE: 19-NOV-1993 CLASSIFICATION ONTA: APPLICATION NUMBER: US 07/991,997 FILING DATE: 17-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/963,308 FILING DATE: 16-OCT-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/888,178 FILING DATE: 26-MAY-1993 PRIOR APPLICATION DATA: APPLICATION THE APPLICATION DATA: APPLICATION THE APPLICATION GENERAL INFORMATION: APPLICANT: Beach, APPLICANT: Xiong, TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses TITLE OF INVENTION: Related Thereto NUMBER OF SEQUENCES: 6 NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: MII-026 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400 TELEPAX: (617) 227-5941 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD SEQUENCE CHARACTERISTICS: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: UZIP: 02109 STREET: LENGTH: Boston amino acid ΜA 148 amino acids 60 State Street USA Floppy disk Yue David 4..

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Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                                                                                                                                      TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PATENTIN Relei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: 06-FEB-199
CLASSIFICATION: 435
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                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS: LENGTH: 148 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                           NAME: FOX, Samuel L.

REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0500000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: InK4c-p18 and InK4d-P19, Inhibitors of TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                 1 MEPSADWLATAAARGRVEEVRALLEAVALPNADNSYGRRPIQVMMMGSARVAELLLLHGA 60
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MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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Hirai Ph.D., Hiroshi
Okuda, Tsukasa
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                                                                 Score 760; DB 3;
Pred. No. 1.6e-83;
Mismatches 0;
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Pred. No. 1.6e-83;
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REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0500000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 202-371-2600
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US-08-384-106A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: ease #1.0, Version #1.30
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
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APPLICANT: Downing M.D., James
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: InK4c-p18 and InK4d-p19,
TITLE OF INVENTION: Cyclin Dependent Kinases
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
121
            121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                                                                  1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                              EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                              MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                            EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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o. 6033847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       1: 148 amino acids amino acid
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                                                                                                                                                                                                  100.0%; illarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                     0;
                                                                                                                                                                                                  Score 760; DB 3;
Pred. No. 1.6e-83;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibitors of CDK4 and CDK6,
                                                                                                                                                                                                                                    Length 148;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                  0;
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RESULT

PCT-US93-09945-4

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PCT-US93-09945-4
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GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Juence 2, Application US/08627610 tent No. 5919997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 17-DEC-1992 FORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                             TITLE OF INVENTION: TRATIFLE OF INVENTION: REVUIRES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Serrano, Manuel APPLICANT: DePinho, Ronald A.
                                                                                                                                                                                                                                                                                                                                                                                                                               -627-610-2
                                                                                                                                                                                                                                                                                                                                                          PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0' FILING DATE: 16-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                   COMPUTER:
                                                                                                                                     ZIP: 02109
                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                             STREET:
APPLICATION NUMBER: US/08/627,610 FILING DATE: 04-APR-1996
                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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                                                                                                                                                                          MA
                                                                                                                                                                                                               60 State Street
                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                        Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASCII(text)
                                                                                   IBM PC compatible
                                                                                                                                                                                                                                  LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 760; DB 5; 100.0%; Pred. No. 1.6e-83;
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                                                                                                                                                                                                                                                                                    Transgenic Animals Having Modified Cell-Cycle Regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 07/991,997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 148;
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; MOLECULE TYPE: protein US-08-627-610-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 227-59. INFORMATION FOR SEQ ID NO:
                                                                                                                    COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-194
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Mathew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
                             TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Serrano, Manuel APPLICANT: Hannon, Gregory J. TITLE OF INVENTION: Call-Cycle Regulatry Proteins, and Uses TITLE OF INVENTION: Related Thereto
                                                                                     TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                              ADDAMESTREET: U. STREET: U. Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
TYPE: amino acids
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                                                                      (617) 227-7400
(617) 227-5941
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                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                               CSI-001CP2
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Pred. No.
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TOPOLOGY:

Length 156; Indels

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Gaps

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APPLICANT: I
APPLICANT: I
APPLICANT: I
       TELECOMMUNICATION INFORMATION: TELEPHQNE: (617) 832-1000
                                                                                                  FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     APPLICATION NUMBER: US 07/991
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963
                                                                                                                                                                                                                FILING DATE: 18-NOVEMBER-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01 FILING DATE: 25-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                       REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/:
FILING DATE: 14-APRIL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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Serrano, Manuel
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                                                                              Matthew P.
                                                                                                                                                                                                                                                                                                                                                                  US 08/248,812
                                                                                                                                     US 07/963,308
                                                                                                                                                                                               US 07/991,997
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US-08-581-918A-2
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-893-274-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                   FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel I.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
                                 PRIOR APPLICATION DATA:
                                                                                                                                             FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPad
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/497,214 FILING DATE: 30-JUN-1995
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
APPLICATION NUMBER: FILING DATE: 18-NO
                                                       FILING DATE:
                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                     14-APR-1994
                                                                                                                                                                                                                                                                                                                                                          02-JAN-1996
18-NOV-1993
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                                                                                                                                                                                                                                              US 08/346,147
             US 08/154,915
                                                                      US 08/227,371
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

us 07/991,997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
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              PRIOR APPLICATION DATA:
                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                      APPLICATION NUMBER: FILING DATE: 29-NOV CLASSIFICATION: 514
                                                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: WordPac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
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APPLICATION NUMBER:
                                  APPLICATION NUMBER: US 0 FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                COUNTRY:
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GY: linear
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                                                                                                                                                                                                           WordPad
                                                                                                                                                                                                                                           IBM PC compatible
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29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        David H.
                                                                                                                                                                                                                           PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                      47
US 08/227,371
                                                  US 08/248,812
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RESULT 10
US-08-822-936-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOOS PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Polyak, Kornelia TITLE OF INVENTION: Isolated TITLE OF INVENTION: Molecule
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FILING DATE: 18-NOV-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079.05
TELECOMMUNICATION INFORMATION:
                                                                                      APPLICATION NUMBER: US/08/822,936 FILING DATE: 21-FEBRUARY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roberts, James M. APPLICANT: Koff, Andrew
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                            CITY: Boston
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                                                                          NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                        ZIP: 02109-2170
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EPNCADPATLTRPYHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley, Hoag & Eliot STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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ilarity 100.0%;
Conservative 0
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(617) 832-1000
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                                                                                                                                                                                                                                                                                                                                                                                                       Isolated P27 Protein, Nucleic Acid
Molecules Encoding Same, Methods of
and Uses of Said Agents
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                                                                                                                                                                                                                                                                                                                                                                   Hoag & Eliot, LLP
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ER: MIV-071.04
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Pred. No. 1.7e-83;
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PCT-US95-04636-2
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Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US U8/300,...
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/248,812
                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                            TYPE: amino acid TOPOLOGY: linear
                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0:
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US95/04636 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 68
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                                                                  Conservative
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Related Thereto
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                                                             Score 760; DB 5;
Pred. No. 1.7e-83;
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Pred. No. 1.7e-83;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-589-981-2
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US-08-589-981-2
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APPLICANT: Gyuris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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APPLICANT: Beach, David H.
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
TITLE OF INVENTION: and Uses Related Thereto
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CORRESPONDENCE ADDRESS:
364 YLRAAAGGTRGSNHARIDAAEGPSDIPD
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                               121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                  61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/589,981 FILING DATE:
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                                                                                                                                                      1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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                                                                 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR
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Pred. No. 6.1e-83;
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RESULT 13 US-08-474-177-2

Sequence 2, Application US/08474177 Patent No. 5624819

SENERAL INFORMATION:

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PRIOR APPLICATION DATA:
08/227,369
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APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1995
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CORRESPONDENCE ADDRESS:
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NAME: Ihnen, Jeffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                       FORMATION FOR SEQ ID NO:
|SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
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                121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 14-APR-1994
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                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                        EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                            MEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 68
                                                                 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
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                                                                                                                                                                                                                 Conservative
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.2e-82;
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SOFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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PRIOR APPLICATION NUMBER: US 08/214,582
APPLICATION NUMBER: US 08/214,582
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APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
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FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
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APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
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129
                                    121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 156 amino acids
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                                                                       69
                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
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                                                                                                                                                 MEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 68
                                                                                           EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                       EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                                                                       al Similarity
147; Conserv
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US-08-480-810-2

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Best Local Similarity
Matches 147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION UMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
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MEDIUM TYPE: Floppy disk
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121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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ZIP: 20005
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                                  EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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Db 129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156

Search completed: September 19, 2002, 17:24:00 Job time: 58 sec

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Scoring table:
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-627-610-2
US-08-93-274-2
US-08-93-274-2
US-08-981-918A-2
US-08-846-1478-2
US-08-842-936-2
US-08-842-936-2
US-08-848-10-2
US-08-487-033-2
US-08-480-810-2
US-08-480-810-2
US-08-480-810-2
US-08-480-810-2
US-08-480-810-2
US-08-480-810-2
US-08-848-251-2
US-08-480-810-2
US-08-155-2
US-09-120-130-2
US-09-120-131-2
US-09-120-131-2
US-08-910-722-2
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US-08-384-106A-16

US-08-384-106A-24

PCT-US93-09945-4
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280.449 Million cell updates/sec
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ALIGNMENTS

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RESULT 1
US-08-154-915-4
                                                                                                                                                                                                     Sequence 4, Application US/08154915
Patent No. 5618669
GENERAL INFORMATION:
APPLICANT: Beach, David
APPLICANT: Xiong, Yue
TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses
TITLE OF INVENTION: Related Thereto
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                              CITY:
STATE:
                                                                                                                                    STREET:
                                                                           Boston
E: MA
PRY: USA
                                                                                                                                      60 State Street
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CURRENT APPLICATION DATA:

19-NOV-1993

US/08/154,915

OPERATING SYSTEM:

PC-DOS/MS-DOS

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      GENERAL
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                               TITLE OF INVENTION: Ink4c-pl8 and Ink4d-Pl9, Inhibitors of TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6
                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                  APPLICANT:
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LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-MAY-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/888,178

FILING DATE: 26-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514

FILING DATE: US 07/701,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CCT-1993
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                            COUNTRY:
                                                                                                                                STREET:
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                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                           20005
                                                                                                             Washington
                                                                                              D.C.
                                                                                                                              E: STERNE, KESSLER, GOLDSTEIN & FOX 1100 New York Ave., N.W.
                                                                                                                                                                                                                                            Hirai Ph.D., Hiroshi
Okuda, Tsukasa
                                                                            USA
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100.0%; Pred. No. 1.4e-130;
tive 0; Mismatches 0;
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Matches
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GENERAL INFORMATION:
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                                                     APPLICATION NUMBER: US/0
FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: In44c-p18 and InK4d-p19, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sherr Ph.D., (APPLICANT: Downing M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS,
SOFTWARE: Patentin Releas
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 06-FEB-1994
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                 NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                    STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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nes 148; Conserv
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TELEFAX: 202-371-2540
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REFERENCE/DOCKET NUMBER: 0656.0500000
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                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 amino acids
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                   0656.0500000
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No. 1.4e-130;
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TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:

202-371-2540

24:

202-371-2600

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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-384-106A-24
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                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US93-09945-4
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PCT-US93-09945-4
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                  Matches 148;
                                                                                                                                                                            Query Match
                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Cyclin
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 16-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                             61
                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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                                                                                    148;
                                                EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                               EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                100.0%; Score 148; DB 5; 100.0%; Pred. No. 1.4e-130;
                                                                                                                                                                                                                                                                                                                                                                                            US 07/963,308
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Pred. No. 1.4e-130;
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                                                                                                                    RESULT 6
US-08-306-511A-2
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Best Local Similarity
Matches 148; Conserv
                                                                                Sequence 2, Application US/08306511A Patent No. 5962316
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                                GENERAL INFORMATION:
APPLICANT: Beach,
APPLICANT: Demetr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Transgenic ATITLE OF INVENTION: Regulation NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: DePinho, Ronald A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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CITY: Boston
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                                                                                                                                                                                                                                                       EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
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GY: linear
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Serrano, Manuel
Hannon, Gregory J.
                                Demetrick, Douglas J.
                                                     Beach, David H.
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                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 148; DB 2; 1 100.0%; Pred. No. 1.5e-130;
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                                                                                                                                                                                                                                                                                           Patent No.
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Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                  APPLICANT: Serrano, Manuel APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, ITILE OF INVENTION: and Uses Related Thereto NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acid
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FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                  121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                  COUNTRY: U
                                                                                               CITY: Boston
                                                                                                         ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
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CITY: Boston
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                                                                                                                                                                                                                                                          Beach, David H.
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IBM PC compatible
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                                                                                                                                                                                                                                           Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/306,511A
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Pred. No. 1.5e-130;
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US-08-581-918A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 148; Conserv
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Best Local
                                                                                                                                                                                       GENERAL INFORMATION:
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INFORMATION FOR SEQ
                                                   APPLICANT: Serrano, Manuel APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                    APPLICANT: Beach, David H. APPLICANT: Demetrick, Doug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/963
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
2700
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APPLICATION NUMBER:
FILING DATE: 25-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                             121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEPSADWLATAAARGRVEEVRALLEAVALPNADNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                     EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
E: Foley, Hoag & Eliot
One Post Office Square
                                                                                                                                                    Demetrick, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.5e-130;
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Gaps

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

02-JAN-1996

US/08/581,918A

CLASSIFICATION:

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

SOFTWARE: COMPUTER:

WordPad

COMPUTER READABLE FORM:

02109 M

USA

MEDIUM TYPE:

Floppy disk

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Sequence 2, Application US/08346147B Patent No. 6211334
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
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FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 07/001 007
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APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 148; DB 3; 100.0%; Pred. No. 1.5e-130;
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RESULT 10
US-08-822-936-2
; Sequence 2, Application US/08822936
; Patent No. 6242575
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Best Local
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INFORMATION FOR SEQ
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 25-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 14-APR-1994
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ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
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LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07
FILING DATE: 17-DEC-1992
ATTORNEY_AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
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APPLICATION NUMBER: U
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                                                                                                                 129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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REFERENCE/DOCKET NUMBER: MIV-071.04
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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RESULT 11
PCT-US95-04636-2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,936
FILING DATE: 21-FEBRUARY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                  TITLE OF INVENTION: Cell-Cycle Regu
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
                                  SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: Isolated P27 Protein, Nucleic Acid
TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acting
TITLE OF INVENTION: and Uses of Said Agents
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ADDRESSEE: Foley, Hoag & Eliot, LLP
STREET: One Post Office Square
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        FILING DATE:
                      APPLICATION NUMBER:
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ZIP: 02109-2170
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Roberts, James M.
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                                                                                                                                                       Cell-Cycle Regulatory Proteins, and Uses Related Thereto
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100.0%; Pred. No. 1.5e-130;
                      PCT/US95/04636
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Best Local S
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                 TELEPHONE:
                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                    STATE:
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(617) 22
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Sequence 2, Application Patent No. 5672508
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beach, David H.
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                                                                                                                                          US/08/589,981
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                      MII-069
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 18-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, Suite 1000
ATTORNEY/AGENT INFORMATION: NAME: Ihnen, Jeffrey L.
                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                            FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cannon-Albright, Lisa A. APPLICANT: Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 07-JUI CLASSIFICATION: 43
                                                                                           FILING DATE: 14-APR-1994
                                                                                                             APPLICATION NUMBER:
                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1201 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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                                                                                                               US 08/227,369
                                                                                                                                                                                                                             US 08/215,087
                                                                                                                                                                                                                                                                                  US 08/251,938
                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/474,177
                                                                                                                                                                     US 08/215,086
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Patent No. 5
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Best Local Similarity
Matches 121; Conserv
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                                                                                                                                 APPLICATION NUMBER: 1
FILING DATE: 18-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                    APPLICATION NUMBER: US 01-JUN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                PRIOR APPLICATION DATA:
                                                               APPLICATION NUMBER: US 01
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: 202-962-4810
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LENGTH: 156 amino acids
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APPLICATION NUMBER: US C
FILING DATE: 18-MAR-1994
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                                                   FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                   14-APR-1994
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              US 08/214,582
                                                                   US 08/227,369
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                                                                                                                    US 08/215,086
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24884-109348-C

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                             FILING DATE: 18-MAK-1337
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/215,086
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: LAVI
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 246
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 36
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LENGTH: 156 amino acids
                                                                    PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/I
FILING DATE: 17-MAR-1995
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MEDIUM TYPE: Floppy
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                                                 APPLICATION NUMBER:
                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 18-MAR-1994
                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
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                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/480,810 FILING DATE: 07-JUN-1995
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                                  14-APR-1994
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                                                                                                                                                                                                                       US 08/251,938
                                                     US 08/227,369
                                                                                                                                                                  US 08/215,087
                                                                                                                                                                                                                                                                            PCT/US95/03316
US 08/214,582
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Best Local Similarity
Matches 121; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/
APPLICATION NUMBER: PCT/US95/
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
TTANTON NUMBER: US to
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Application in the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 156 amino acids
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ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                           REFERENCE/DOCKET NUMBER:
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5. 5843756
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100.0%; Pr
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Pred. No. 2.1e-105;
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION:
                                                                  FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                         FILING DATE: 18-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                 PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                  APPLICATION NUMBER: FILING DATE: 14-API
                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
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 APPLICATION NUMBER:
                                                                                                        APPLICATION NUMBER:
                                                                                                                                                              APPLICATION NUMBER: US 08/215,087
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
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                                    14-APR-1994
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100.0%; Pred. No. 2.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERMLINE MUTATIONS IN THE MTS GENE AND METHOD FOR DETECTING PREDISPOSITION TO CANCER AT GENE
                                                     US 08/227,369
                                                                                                          US 08/215,086
                                                                                                                                                                                                                                                                                                              US 08/474,083
                                                                                                                                                                                                                                                                        PCT/US95/03537
US 08/214,582
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Best Local
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INFORMATION FOR SEQ ID NO:
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                                                            PRIOR APPLICATION UNMBER: US 08,
PRIOR APPLICATION NUMBER: US 08,
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08,
APPLICATION NUMBER: US 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                 APPLICATION NUMBER: US 08/251,938
                                                                                                                                                                                                                                                      FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
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                                               FILING DATE:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
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01 New York Avenue, Suite 1000
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14-APR-1994
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                                                               US 08/215,086
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              US 08/227,369
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; Pred. No. 2.1e-105;
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          APPLICATION NUMBER: US 08,
EILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 18-MAR-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC pc5/MS-Dos
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                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 01-JUN-1994
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                                                                                                                                                                                     FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                   APPLICATION NUMBER:
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202-962-8300
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                            us 08/215,086
                                                                     US 08/215,087
                                                                                                               us 08/251,938
                                                                                                                                                          08/480,810
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RESULT 20
US-09-115-252-2
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US-09-120-130-2
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Best Local :
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FILING DATE: 01-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                       PRIOR APPLICATION DATA:
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                                                                                FILING DATE: 07-JUN'LL'
APPLICATION NUMBER: PCT/U
APPLICATION TOMBER: PCT/U
TTTNG DATE: 17-MAR-1995
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                                       APPLICATION NUMBER: US 08/251,938 FILING DATE: 01-JUN-1994
                                                                                                                             APPLICATION NUMBER: US/08/480,810 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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   US 08/215,087
                                                                                                            PCT/US95/03316
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FILING DATE: 18-MAR-PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
APPLICATION NUMBER:

18-MAR-1994

US 08/215,086

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TOPOLOGY: 1i;
MOLECULE TYPE:
US-09-115-252-2
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                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MTS1 GENE NUMBER OF SEQUENCES: 36
                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                          CLASSIFICATION:
                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
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               APPLICATION NUMBER: US 0 FILING DATE: 01-JUN-1994
                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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100.0%; Pred. No. 2.1e-105;
ative 0; Mismatches 0;
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                                    US 08/251,938
                                                                                                                                                          US/08/986,515
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-986-515-2
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; Sequence 2, Applic
; Patent No. 6140473
ETLING APPLICATION:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
TTING DATE: 17-MAR-1995
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SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                              STREET: 1201 New CITY: Washington
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                                                                                                                                      APPLICATION NUMBER: US/09/120,128 FILING DATE:
                                                                                                                                                                                                                                                                                          ZIP: 20005
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100.0%; Pred. No. 2.1e-105;
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US 08/486,047

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              LT 23
9-120-129-2
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INFORMATION FOR SEQ
                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,129
FILING DATE:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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LENGTH: 156 amino acidi
PRIOR APPLICATION DATA
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APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/214,582 FILING DATE: 18-MAR-1994 ATTORNEY/AGENT INFORMATION:
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                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 D 156
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                                                                                                                                                                                                  CITY: Washington
STATE: DC
                   CLASSIFICATION:
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
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100.0%; Pred. No. 2.1e-105;
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                                                                                                                                                                                                                                                                                                              Patent No. 6210949
GENERAL INFORMATION:
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Matches 121; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                             APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
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                                                                               COUNTRY: US
ZIP: 20005
                                                                                                                                   CITY: Washington
                                                                                                                                                           STREET:
                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/214,582 FILING DATE: 18-MAR-1994
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FILING DATE: 17-MAR-1995
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18-MAR-1994
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18-MAR-1994
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100.0%; Pred. No. 2.1e-105;
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PatentIn Release #1.0, Version #1.30

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US-09-120-131-2
; Sequence 2, Application US/09120131
; Patent No. 6218146
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Best Local Similarity
Matches 121; Conserv
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LENGTH: 156 amino acids
TYPE: amino acid
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APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        NERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TOPOLOGY:
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STREET: Washington
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TELEFAX: 202-962-8300
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                                                                                        CLASSIFICATION:
                                                                                                         FILING DATE
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US-09-120-131-2
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Patent No. 6251871
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
myve: Telepolical
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
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FILING DATE: 18-MAR-1994
ATTORREY/AGENT INFORMATION:
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APPLICATION NUMBER: US OF
                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        APPLICANT: Jin, Xiaomei
APPLICANT: Roth, Jack A.
TITLE OF INVENTION: pl6 EXPRESSION CONSTRUCTS AND THEIR
TITLE OF INVENTION: APPLICATION IN CANCER THERAPY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ZIP: 77210
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CITY: Houston
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APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                 Texas
                                                                                                                                                                                                                                 E: Arnold, White & Durkee P.O. Box 4433
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                                                                                                                                                                            United States of America
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100.0%; Pred. No. 2.1e-105;
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                  us/08/910,722
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Best Local Similarity
Matches 121; Conserv
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                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          ZIP: 2000
COMPUTER READABLE FORM:
COMPUTER FLOPPY disk
                                                                                                                                                                                             SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 D 148
                                 APPLICATION NUMBER: US 0 FILING DATE: 01-JUN-1994
 APPLICATION NUMBER:
                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 ALPNAPNSYGRRPIQYMMMGSARVAELLLLHGAEPNCADPATLTRPYHDAAREGFLDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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TELEX: 79-0924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Washington
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100.0%; Pred. No. 2.1e-105;
                                                  US 08/251,938
                                                                                                                                                                            US/08/474,177
US 08/215,087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08487033 Patent No. 5739027
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
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                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kamb, Alexander TITLE OF INVENTION: MTS1E1
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LENGTH: 105 amino acids
TYPE: amino acid
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APPLICATION NUMBER: 1
FILING DATE: 18-MAR-
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                                                 APPLICATION NUMBER: FILING DATE: 01-JUI
                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28
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                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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01 New York Avenue, Suite 1000
                                                 01-JUN-1994
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18-MAR-1994
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                 US 08/215,087
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RESULT 29
US-08-480-810-14
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Best Local Similarity
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/I FILING DATE: 17-MAR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                       PRIOR APPLICATION DATA:
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487-033-14
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APPLICATION NUMBER: US US TO THE THE TOTAL THE
                                                                                                                                                                                                            APPLICATION NUMBER: US 0: FILING DATE: 01-JUN-1994
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STATE: DC
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SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
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                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US to be assigned
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/508,735
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                                                                                                                                                          APPLICATION NUMBER: US to FILING DATE: 07-JUN-1995
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Kamb, Alexander
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IBM PC compati
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)1 New York Avenue, Suite 1000
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18-MAR-1994
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
mypre. Ento acids
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APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
                                                                                                                                                                                                     FILING DATE: 01-JUN-1994 PRIOR APPLICATION DATA:
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PRIGR APPLICATION DATA:
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FILING DATE: 07-JUN
APPLICATION NUMBER:
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                                 APPLICATION NUMBER:
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1201 New York Avenue, Suite
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INFORMATION:
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18-MAR-1994
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Pred. No. 1.1e-90;
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US-08-486-047-14
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GENERAL INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            FILING DATE: 17-MAR-PRIOR APPLICATION NUMBER:
                                             ATTORNEY/AGENT INFORMATION:
                                                                                           PRIOR APPLICATION DATA:
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                                                              FILING DATE:
                                                                                                           FILING DATE:
                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/0
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/UN APPLICATION NUMBER: US/UN PTILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Washington
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                                                                           APPLICATION NUMBER:
                                                                                                                                                          FILING DATE: 18-MAR-1994
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                 REGISTRATION NUMBER:
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                           Jeffrey L.
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NUMBER:
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Pred. No. 1
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Best Local Similarity
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                                                                       APPLICATION NUMBER: US 08/214,582 FILING DATE: 18-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                 FILING DATE: 14-APR-1994 PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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OPERATING SYSTEM:
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                                                 NAME: Ihnen, Jeitre REGISTRATION NUMBER:
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1201 New York Avenue,
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SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ATTORNEY/AGENT INFORMATION:
NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                    FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                        UMBER: US 08/251,938
01-JUN-1994
                                                                                                          UMBER: US 08/214,582
18-MAR-1994
                                                                                                                                                                                                                 18-MAR-1994
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17-MAR-1995
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Patent No. 6090578
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, Suite 1000
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LENGTH: 105 amino acids
TYPE: amino acid
                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
            TELEPHONE: 202-962-4810
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CTTY: Washington
                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 18-MAR-1994
                                                          NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                               FEFERENCE/DOCKET NUMBER:
                                                                                                                                                                    FILING DATE: 14-APR-1994
                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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202-962-8300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1.1e-90;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-986-515-14
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US-09-120-128-14
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APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/486,047
                 TELECOMMUNICATION INFORMATION:
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LENGTH: 105 amino acids
                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                    APPLICATION NUMBER: US (FILING DATE: 18-MAR-1994
                                                  NAME: Ihnen, Jeffre REGISTRATION NUMBER:
                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 14-AP
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 01-JUN
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE:
                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUI APPLICATION NUMBER:
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                                                              Jeffrey L.
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Pred. No.
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SEQUENCE CHARACTERISTICS:

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Best Local Similarity
Matches 105; Conserv
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Patent No. 6180776
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INFORMATION FOR
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, Suite 1000
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                            REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                         FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/214,582
FILING DATE: 18-MAR-1994
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MEDIUM TYPE: Floppy disk
                                                                                                                      ATTORNEY/AGENT INFORMATION:
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TOPOLOGY:
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                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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amino acid
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                 202-962-8300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US95/03316
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                                                                                                                                                                                                                  US 08/227,369
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                                                                                      28,957
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RESULT 38
US-09-201-139-14
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; MOLECULE TYPE: US-09-201-139-14
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Best Local Similarity
Matches 105; Conserv
                                                                                     INFORMATION FOR SEQ ID NO:
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LENGTH: 105 amino acids
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                         NAME: Ihnen, Jeffrey REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                            TOPOLOGY:
                                           TYPE:
                                                                                                               TELEPHONE:
                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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Kamb, Alexander
                                                         105 amino acids
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                  202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
             protein
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Pred. No. 1.1e-90;
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Query Match 70.9%; Score 105; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-90; Matches 105; Conservative 0; Mismatches 0;

Length 105;

Indels

0;

Gaps

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; MOLECULE TYPE: US-09-120-131-14
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                  Query Match 70.9%; Sc
Best Local Similarity 100.0%; F
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                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 18-MAR-:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kamb, Alexander TITLE OF INVENTION: MTS2 G
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                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                      NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/251,938 FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US UN APPLICATION NUMBER: US UN APPLICATION DATE: 07-JUN-1995
                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 01 FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/UFILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                 amino acid
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                                                                                                                                    linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                             NUMBER: US 08/214,582
18-MAR-1994
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                                      Score 105;
Pred. No.
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                     Mismatches
                                    1.1e-90;
                                                    DB 4;
                     0,
                                                 Length 105;
                   Indels
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              Gaps
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                             RESULT 41
US-08-581-918A-37
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Sequence 37, Application US/08581918A Patent No. 6043030
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein LOCATION: 1..157 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One marker CITY: San Francisco
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CLASSIFICATION:
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(415) 543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                             157 amino acids
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llarity 100.0%;
Conservative 0;
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17-APR-1995
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
123 GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD
                     114 GHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 LLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEEL 122
                                                                                                54 LLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEEL 113
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One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                     /note= "human p16"
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                                                                                                                                                                                Score 95; DB 5; L; Pred. No. 3.4e-81;
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157
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                                                                                                                                             Query Match
Best Local Similarity
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TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-NOV-1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/497,214
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                                                                                                                                                                                                                                     MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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                              101 AWGRLPVDLAEELGHRDVARYLRAAAGGT 129
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 29-NC
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                 IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 100
AWGRLPVDLAEELGHRDVARYLRAAAGGT 89
                                                               IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 60
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One Post Office Square
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                                                                                                                                  Conservative
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SYSTEM: PC-DOS/MS-DOS
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14-APR-1994
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                                                                                                                               60.1%; Score 89;
100.0%; Pred. No.
tive 0; Mismatc
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                                                                                             Matches
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  TELEPHONE: (617) 832-
TELEFAX: (617) 832-70
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
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APPLICATION NUMBER:
FILING DATE: 14-SEP-
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FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION
NAME: VINCOL Matthew D
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 101 AWGRLPVDLAEELGHRDVARYLRAAAGGT 129
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SOFTWARE: WORDPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 100
                                IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 60
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One Post Office Square
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Demetrick, Douglas J.
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                                                                                             Conservative
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                                                                                                                                                                                                       linear
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14-APR-1994
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29-NOV-1994
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18-NOV-1993
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Cell-Cycle Regulatory Proteins,
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                                                                                                        60.1%;
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SER: MIV-071.04
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                                                                                                          Score 89;
Pred. No.
                                                                                             Mismatches
                                                                                     DB 4; Lc
o. 7.7e-76;
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AWGRLPVDLAEELGHRDVARYLRAAAGGT 89

Patent No. 6043030 GENERAL INFORMATION:

APPLICANT: Beach, David H.

Demetrick, Douglas J.

TITLE OF INVENTION:

APPLICANT:

Serrano, Manuel Hannon, Gregory J. WENTION: Cell Cycle Regulatory Proteins,

Uses

Related Thereto

CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Foley, Hoag & Eliot One Post Office Square

STREET: One F

NUMBER OF SEQUENCES:

08-581-918A-38

Application US/08581918A

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                                                                                                     ; TOPOLOGY: 1;; MOLECULE TYPE: US-08-581-918A-38
                              Matches
                                                           Query Match
                                                                                                                                                                                                          TELEFAX: (617) 832-70 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08,
EILING DATE: 25-MAY-177
RIOR APPLICATION TO NUMBER: US 08,
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41 IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 100
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 14-APR-1994
                              Local Similarity es 72; Conserv
                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                           : 88 amino acids amino acid
                           48.6%; ilarity 100.0%; Conservative
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                                                                                                                   peptide
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17-DEC-1992
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80: 38:
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                                           Score 72;
Pred. No.
                              0
                              Mismatches
                     DB 3; LC.
5.2e-60;
0;
                                                        Length 88
                             Indels
                           0;
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RESULT 44
US-08-346-147B-38
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                                                                                TELEFAX: (617) 832-700
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                 FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 17-DEC-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPad
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TOPOLOGY: 11
                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                  STRANDEDNESS
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                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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STREET: One Post Office Square
                                                                   LENGTH:
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                                                  amino acid
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                   linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  (617) 832-1299
peptide
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25-MAY-1994
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                                                                                                                                                                                 36,709
                                                                                                                                                                   MIV-071.04
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PRIOR APPLICATION DATA:
APPLICATION MABER: US 08/:
FILING DATE: 29-NOV-100

US 08/346,147

CIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 30-JUN-1

US 08/497,214

CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPad

APPLICATION NUMBER: FILING DATE: 02-JAN CLASSIFICATION: 435

02-JAN-1996

US/08/581,918A

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

COUNTRY: USA ZIP: 02109

ΑM

Matches Query Match Best Local (

Similarity 100. 72; Conservative

48.6%; 100.0%;

Score 72; Pred. No. Mismatches

DB 4; .o. 5.2e-60; 0;

Length 88 Indels

0;

Gaps

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RESULT 46
US-08-306-511A-4
Sequence 4, Application US/08306511A
; Patent No. 5962316
                                                                                                                                                                                                                               Query Match
Best Local Similarity
"-+-hes 72; Conserv?
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 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..136
OTHER INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: Not y
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 100
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100.0%; Pro
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Pred. No.
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                                                                                                                                                                                                                                                                                               Patent No.
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Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08893274
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                           APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
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                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HC
                                                                                                                                                                                                                                            APPLICANT: APPLICANT:
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TITLE OF INVENTION: Cell-Cycle Regulatry Proteins,
TITLE OF INVENTION: Related Thereto
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                                                  ZIP:
                                                                COUNTRY:
                                                                                              CITY: Boston
                                                                                                               STREET:
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                                                                                                                             ADDRESSEE:
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Demetrick, Douglas J.
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227-5941
                                                                                                                              HOAG & ELIOT LLP
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100.0%; Pred. No.
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US-08-474-177-16
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Best Local Similarity
"arches 72; Conserva
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                            APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
                                                                                                                                                    CORRESPONDENCE ADDRESS:
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FILING DATE: 25-MAY-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963
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ATTORNEY/AGENT INFORMATION:
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                                                                               CITY: Washington
STATE: DC
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                                                    COUNTRY: USA
ZIP: 20005
                                                                                                                     STREET:
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FILING DATE: 18-NOVEMBER-1993
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                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: MIV-071.09
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                                                                                                                 1201 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.6%; Score 72; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                 Venable, Baetjer, Howard & Civiletti, LLP 01 New York Avenue, Suite 1000
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Best Local :
                                                                                 COUNTRY: UZIP: 20005
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; MOLECULE TYPE: US-08-474-177-16
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COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                             APPLICANT: Kamb, Alexander TITLE OF INVENTION: MTS1E1
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,
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APPLICATION NUMBER: US 0
FILING DATE: 14-APR-1994
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CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:

CLASSIFICATION:

APPLICATION NUMBER: PCT/TFILING DATE: 17-MAR-1995

PCT/US95/03316

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-UU-1995

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US-08-480-810-16; Sequence 16, Application US/08480810; Patent No. 5801236
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Best Local Similarity
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TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC roos/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
                                                                                                                                                                                                                           APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 14-APR
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TOPOLOGY: linear
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                                                                                                                                                                          CITY: Washington
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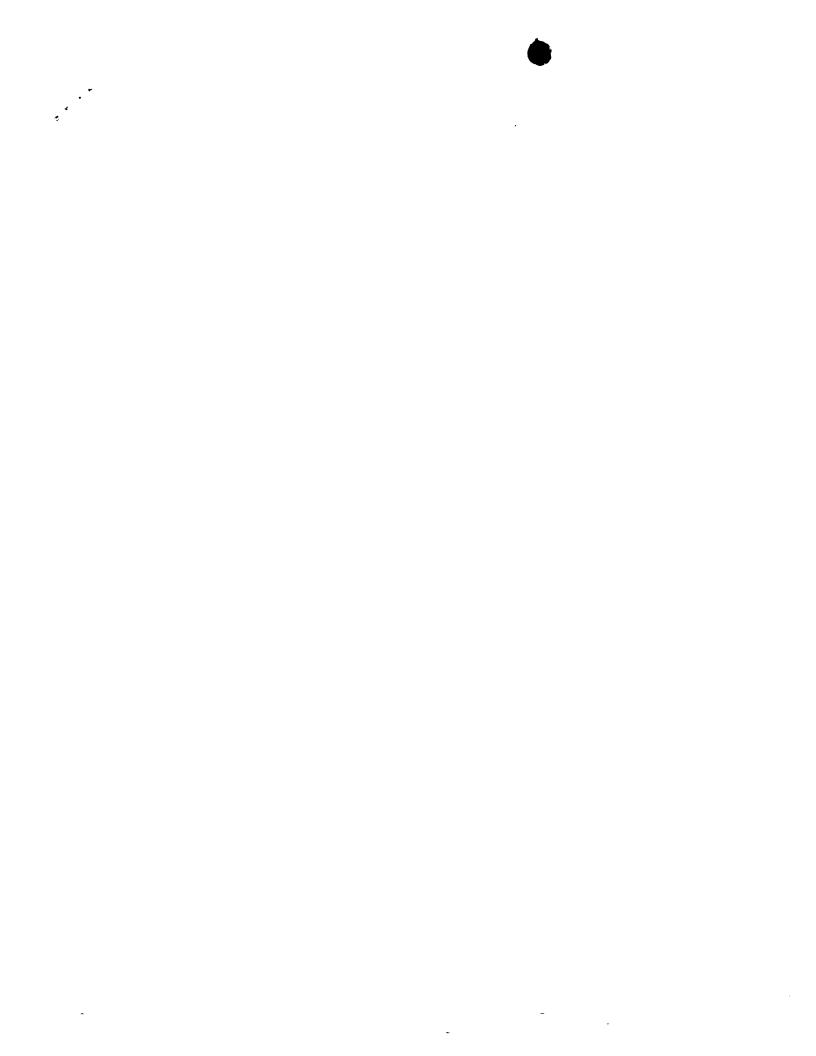
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LENGTH: 138 amino acids
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APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
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               101 AWGRLPVDLAEE 112
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AWGRLPVDLAEE 122
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 Mismatches

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Pred. No.
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Search completed: September 19, 2002, 17:28:51 Job time: 219 sec



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/SIDS1/gcgdata/hold-gèneseq/geneseqp-emb1/AA1981.DAT:*
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AAR81701
AAR80940
AAR85116
AAR85116
AAY24741
AAY88354
AAW95094
AAW95094
AAY97526
AAY96068
                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                       Human INK-4 protei
Human cell cycle r
CDK inhibitory fus
Human p27-p16 fusi
Human W3 protein s
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Human multiple tum
Inhibitor of cycli
Cell-cycle regulat
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Angiogenesis
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n MTS1E1beta p n multiple tum n multiple tum n multiple tum

ALIGNMENTS

RESULT
AAR81701
ID AAR8
XX AAR81701 standard; Protein; 148 AA

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RESULT
AAR80940
ID AAR8
XX
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DT 03-M
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
03-MAY-15-96
                    AAR80940;
                                                                                                                                                                                                                                                                                                        An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS1 gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
                                        AAR$0940 standard;
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Detecting polymorphism associated with cancer pre:disposition - \cdot DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening
                                                                                                                                                                                                                                                                                                                                                                                      Example 8; Pages 92-93; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT00736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cannon-Albright LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multiple tumour suppressor; MTS1; cancer; diagnosis; assay; predisposition; melanoma; leukaemia; lymphoma; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYRI-) MYRIAD GENETICS INC (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9525813-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreas; breast; thyroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multiple tumour suppressor 1 (MTS1) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-1996
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                                                                                                                                                                             YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                  EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLFVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1995-344626/44.
                                                                                                                                                                                                                                                                                                     etc..
                                                                                                                                                                                                                                                                                148 AA;
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(first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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94US-0215087.
94US-0227369.
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94US-0214582
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                                       Protein;
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AAR53401
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                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                               Several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence is the MTS polypeptide MTSI must polypeptide MTSI polypeptide MTSI polypeptide MTSI converted diagnosis or prognosis of human cancer. Germ-line mutations of the Storm of the MTS converted for diagnosing predisposition to melanoma, isolated and cancers of the pancreas, thyroid, ovary, uterus, lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer theraponal may be setted for screening for potential cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994;
18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
18-MAR-1994;
18-MAR-1994;
              AAR53401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild-type multiple tumour suppressor - useful in diagnosis, prognosis and melanoma or leukaemia
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 92-93; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-344401/44.
N-PSDB; AAQ99158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multiple tumour suppressor; El-alpha; diagnosis; cancer; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma;
                                                                                    121
                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human multiple tumour suppressor polypeptide, MTS1
                                                                                                                                           61
                                                                                                                                                                       61
                                         ω
                                                                                                                                                                                             MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                 ylraaaggtrgsnharidaaegpsdipd 148
                                                                                                             YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                       EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                         epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar
                                                                                                                                                                                                                                                                    Similarity
           standard;
                                                                                                                                                                                                                                                                                                                             148
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0214581.
94US-0214582.
94US-0215088.
94US-0227369.
94US-0215086.
94US-0215087.
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             Protein;
                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                     Score 148; DB 16;
Pred. No. 1.5e-134;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MTS) gene and mutant see
therapy of human cancer,
                                                                                                                                                                                                                                                                                Length 148;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : leukaemia;
glioma;
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                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of subunit components of cyclin complexes - used for diagnosing transformation of a cell and developing inhibitors activators, partic for cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukae lymphoma; cell cycle; detection; identification; tumour virus; proliferating cell nuclear antigen; subunit; complex.
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9409135-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beach DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1992;
17-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitor of cyclin dependent kinase 4 (p16INK4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR53401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-1993;
 121
                                 121
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                                                                                                                                                                                                      / Match 100.0%;
Local Similarity 100.0%;
nes 148; Conservative (
                                                                   61
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DB; AAQ63491.
                YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                              ylraaaggtrgsnharidaaegpsdipd 148
                                                                                                                                  MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                          weight polypeptides and can therefore of transformation of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 40; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xiong Y;
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92US-0991997.
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                                                                                                                                                                                                        0;
                                                                                                                                                                                                      Score 148; DB 15;
Pred. No. 1.6e-134;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            be used to identify
                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia;
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RESULT
AAR85116
AD AAR85116
AD AAR85116
AC AAR8
AC AAR8
AC AAR8
AC Cell
KW CCR;
XX
CCR;
XX
HOMO
PN WO95
PN WO14
PN WO16
PN WO1
RESULT
AAY24741
ID AAY
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AC AAY
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Best Local 9
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14-APR-1994;
25-MAY-1994;
14-SEP-1994;
                           AAY24741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was obtd. by expression of a cDNA clone (AAR702962) isolated in a 2-hy screening assay. CCR p16 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor; CCR; cancer; cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR85116 standard; Protein; 156 AA.
                                                                            AAY24741 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-373798/48
N-PSDB; AAT02962.
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                                                                                                                                                                                                             129 ylraaaggtrgsnharidaaegpsdipd 156
                                                                                                                                                                                                                                                              121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
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                                                                                                                                                                                                                                                                                                                                             EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR
                                                                                                                                                                                                                                                                                                                                                                                                                          mepsadwlataaargrveevralleavalpnapnsygrrpiqvmmmgsarvaellllhga
                                                                                                                                                                                                                                                                                                                  epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 76-77; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative 0
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94US-0227371.
94US-0248812.
94US-0306511.
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                                                                            Protein; 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148; DB 16;
Pred. No. 1.6e-134;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2-hybrid
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Best Local
                                                                                                                                                                                                                                                                                                     The present invention describes a transgenic mouse having germline and somatic cells which comprise an incorporated transgene that disrupts and inhibits the p16-INK4-a gene leading to tumour susceptibility. Also described is a method of making a mouse and mouse embryonic stem cells a functionally disrupted p16-INK4-a gene which comprises transferring a transgene construct into embryonic stem cells of a mouse and transferring these into a mouse blastocyst and implanting the resulting chimeric blastocyst into a female mouse selecting offspring having an endogenous p16-INK4-a gene allele. The transgenic mouse is useful for evaluating the carcinogenic potential or the anti-proliferative activity of a test compound. The present sequence represents the human INK4 protein p16 given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-1996;
18-NOV-1993;
14-APR-1994;
125-MAY-1994;
14-SEP-1994;
29-NOV-1994;
30-JUN-1995;
02-JAN-1996;
            AAY88354 standard;
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 45-46; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic mice with modified cell-cycle regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beach
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                                                                          129
                                                                                                121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                         69
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                                                                       MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                        EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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148; Conser
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                                                                                                                                                                                                                          Conservative
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YESHIVA EINSTEIN COLLEGE.
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94US-0346147.
95US-0497214.
96US-0581918.
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94US-0227371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p18; p19; CDK4; cell cycle regulatory protein;
p16-INK4-a; carcinogen; anti-proliferative.
            Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA,
                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                       Score 148; DB 20;
Pred. No. 1.6e-134;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                         156
                                                                                                                                                                                                                                               Length 156;
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MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60

Query Match Best Local Matches

hes 148;

Similarity

100.0%; larity 100.0%; Conservative 0

0; Score Pred.

148; DB 21; No. 1.6e-134;

Length

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This sequence represents the human cell cycle regulatory protein (CCR) pl6 amino acid sequence. The pl6 gene is located on chromosome 9p21-22. The invention relates to a diagnostic assay which comprises detecting a mutation in the pl6 gene, which is used to identify a cell or cells at risk of developing a disorder characterised by unwanted cell proliferation or differentiation. Pl6 is a cyclin-dependent kinase (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle progression and ultimately cell growth. The assay can be used for identifying a cell or cells at risk for a disorder (neoplasia) characterized by unwanted cell proliferation or differentiation. The method is used for detecting mutations in either a CCR gene or CDK gene which a the control of the compression of the central proliferation is neither a CCR gene or CDK gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1994;
25-MAY-1994;
14-SEP-1994;
29-NOV-1994;
30-JUN-1995;
                                                which alter complex formation between these two proteins. The method is also used for detecting mutations in other callular proteins which disrupt protein interactions such as mutations which disrupt binding of the p53 protein with other cellular proteins, e.g. Wilm's tumour suppressor protein WT1. They can also be used to detect mutations in pairs of signal transduction proteins such as ras protein or other cellular proteins (GAPs). The method is convenient for detecting mutants of CCR genes encoding proteins which interact with ras, e.g. ras GTPase activating proteins encoding proteins which are unable to physically interact with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory protein) in a diagnostic assay for identifying a cell at risk for disorder characterized by unwanted cell proliferation or
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1992;
18-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Column
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cycle regulatory protein; CCR; p16; diagnostic assay; detection; proliferation; differentiation; neoplasia; cancer; cell growth; in-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-270336/23.
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                                       protein.
   156
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93US-0154915.
94US-0227371.
94US-0248812.
94US-0306511.
94US-0346147.
95US-0497214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      61pp;
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                     degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculitis, and to inhibit spermatogenesis or oogenesis. The chimeric proteins can also be used in vitro to maintain cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK/cyclin complex than binding mottifs used individually (since they may bind to CDK involved in different stages of
                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (cDK) binding motifs from at least two different proteins that bind to CDKs. The protein controls proliferation and/or differentiation of cells, particularly they inhibit cell-cycle progression. They can be used to
                                                                                                                                                                                                                                                                                                          treat a wide range of proliferative disorders, e.g. cancer, leukaemia, psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 40; Page 38-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         herapy of cancer and
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Best Local
The invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic
                                                                                                                                                                                                                 Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transceptosis; vascular wound; repair; halr; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
                                                                                                                                                                        Claim
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                                                                                                                                                                                                   fibrosis and neurodegeneration
                                                                                                                                                                                                                                                                                                                                                         (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tachycardia; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; tumour; inflammation; neurodegeneration; periodontal; spermatogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95094 standard;
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mes 148; Conser
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                                                                                                                                                                                                                                                                                             1999-153770/13
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                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                             DH,
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                                                                                                                                                                                                                                                                                                                           Gyuris J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion protein
                                                                                                                                                                        70-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                    88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurodegeneration; periodontal; spermatogenesis;
                                                                                                                                                                                                                                                                                                                           Lamphere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p16.
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Pred. No. 3.8e-134;
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Also provided are nucleic g: (i) a therapeutic

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RESULT
AAY97526
ID AAY9
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AC AAY9
XX
AC 15-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                     01-MAR-1999;
08-APR-1999;
09-APR-1999;
 N-PSDB; KAA90923
                                                                                                                                                                                                                                                                                              Human W3 protein sequence
                                                                                                                                                                                                                                                                                                                         15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                           AAY97526 standard;
              WPI; 2000-587315/55
                                      Patel S,
                                                                                                                                                       01-MAR-2000; 2000WO-US05350
                                                                                                                                                                                 08-SEP-2000
                                                                                                                                                                                                          WO200052184-A1
                                                                                                                                                                                                                                                          adenovirus E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                   Homo
                                                               (MITO-) MITOTIX INC.
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                                                                                                                                                                                                                                                                       chimeric
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                                                                           CELL GENESYS INC
                                      McArthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                          ric cyclin
protein;
                                                                                                     99US-0122974.
99US-0128271.
99US-0128515.
                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                         dependent kinase inhibitor;
neoplasia; W3 protein.
                                     Gyuris
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Pred. No. 3.8e-134;
; Mismatches 0;
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                                       Mendez
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                                                                                                                                                                                                                                                                      therapy;
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01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
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Qy В δÃ Вb Qy

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cycl dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin depe
pl6; human;
                                                                                           28-FEB-2000; 2000WO-US04971
                                                                                                                                                                                   WO200052159-A1.
                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiproliferative p27-p16 fusion protein W3
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148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4; uman; smooth muscle cell; hyperproliferation; restenosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 108-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiproliferative; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
99US-0122974.
99US-0163682.
99US-0457568.
                                                                                                                                                                                                                                                                                             /label= p27
205..219
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                                                                                                                                                                                                                                                                                                                                                              /label= 6His_tag
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Pred. No. 3.8e-134;
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RESULT 1
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Best Local :
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                                                      Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; INK4; p27; p16; human; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The method is to inhibit mammalian smooth muscle cell hyperproliferation, induced by injury caused by angioplasty, stent placement or vein engraftment. It is useful for treating vascular pathologies e.g., restenosis. Also claimed are recombinant lentiviruses encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Gly4Ser)3 hinge and the human pl6 protein (see AMY96053). It is encoded by a nucleic acid obtained by PCR amplification of p27 and p16 DNAs using primers that also included codons for the tag/hinge regions. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a replication-deficient recombinant adenovirus that lacks functional E1 and E4 regions, and comprises a transgene encoding a cyclin dependent kinase inhibitor (CDKi). The CDKi is selected from an INK4 family protein such as human p16, a CIP/KIP family protein such as p27, active fragments of these, or fusion proteins
           Homo sapiens
                                          antiproliferative; gene therapy
                                                                                                                                                                        05-DEC-2000
                                                                                                                                                                                                                                   AAY96068 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant lentivirus for inhibiting proliferation muscle cells in e.g. restenosis, is replication deficient a transgene encoding a cyclin dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-terminal 6His tag,
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                                                                                                                                                                                                                                                                                                                                                                                EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                    YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                   ylraaaggtrgsnharidaaegpsdipd 391
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                                                                                                                                       (p27-p16 fusion)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finer
                                                                                                                                                                                                                                       391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 148; DB 21;
Pred. No. 3.8e-134;
Mismatches 0;
                                                                                                                                                                                                                                     A
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Query Match Best Local Matches

148;

Conservative

0;

Mismatches

0,

Indels Length

Gaps

0;

303

391; 0;

Similarity

100.0%;

Score 148; DB 21; Pred. No. 3.8e-134;

244

1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60 ${\tt mepsadwlataa} argreevralle avalpnapn sygrrpiq v {\tt mmm} gsarvaelllh garbar argreevralle avalpnapn sygrrpiq v {\tt mmm} gsarvaellh {\tt mmmm} gsarvaellh {\tt mmm} gsarvaellh {\tt$

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CC comprising an N-terminal 6His tag, the human p27 protein W3

C comprising an N-terminal 6His tag, the human p27 protein (see

CC AAY96066), a (Gly4Ser)3 hinge, and the human p16 protein (see

CC AAY96067). The fusion protein is encoded by a nucleic acid (see

CC AAY96067). The fusion protein is encoded by a nucleic acid (see

CC AAY96067). The fusion protein is encoded by a nucleic acid (see

CC AAA960523) that was obtained by PCR amplification of human p27 and p16

CC DNAS using primers that also included codons encoding the tag/hinge

CC regions of the fusion protein. A claimed method for inhibiting

CC anglogenesis involves transducing an epithelial cell with a

CC ransgene encoding a cell dependent kinase inhibitor (CDKi). The

CC delivery system for the transgene is a liposome or a recombinant

CC virus. The CDK i is a protein of the CIP/KIP family such as p27, a

CC protein of the INK4 family such as p16, active fragments of these

CC proteins, or a fusion of 2 CDKi proteins such as p27 and p16. The

CC method is useful in treating conditions associated with angiogenesis,

CC such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis

CC and vascular retinopathy (claimed). Alternatively, the transgene

CC is delivered to an auxiliary cell, and is expressed by that cell

CC condition, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle

CC condition, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 108-110; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1999;
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05-NOV-1999;
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99US-0163682.
99US-0457646.
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205..219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the tumour suppressor p16. The DNA encoding CC this sequence is joined to a promoter functional in eukaryotic cells and used in the expression construct of the invention. p16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the carpession construct inhibits p16 function. Reduced or increased levels of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by containing the containing t
                                                                                                                                                                                                                                   Matches 121;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression construct contg. DNA for tumour suppressor restore pl6 activity to transformed cells, useful for or bladder cancer or melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; cancer cell; lung cancer; bladder cancer; melanoma; restenosianti-angiogenic activity; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-132336/12.
N-PSDB; AAT60951.
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                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   or immunoassay.
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                                                                                                                                                28 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
           96
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                                                                                                                35 alpnapnsygrrpigvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 95
VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                                                                                                                                                                                                                                                                                             156 AA;
                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                             81.8%; Score 121; DB 18; 100.0%; Pred. No. 1.6e-108;
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                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                     Length 156;
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treating
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AAW74549
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AAW19251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
           AAW74549 standard; Protein;
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Query Match
Best Local Similarity
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human multiple tumour suppressor 1 gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW19251 standard; Protein; 156
                                                                                                                                                                                                                                                                             The present sequence the human multiple tumour suppressor 1 (MTS1) gene product, useful in cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-258217/23.
N-PSDB; AAT72311.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cannon-Albright LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MYRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1994;
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                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                         Claim 1; Columns 61-64; 72pp; English
                                                                                                                                                                                                                                                                                                                                                      Human mutant multiple tumour suppressor gene sequences production of recombinant mutant polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                     {\tt 36~alpnapnsygrrpiqvmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv}
a
                                                                                                                                 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
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156
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UNIV UTAH RES FOUND
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94US-0215086.
94US-0215087.
94US-0227369.
94US-0227369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour;
                                                                                                                                                                                          81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kamb A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        suppressor;
                                                                                                                                                                             0;
                                                                                                                                                                                          Score 121; DB 18;
Pred. No. 1.6e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Skolnick MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTS1; cancer; diagnosis
                                                                                                                                                                             c
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                                                                                                                                                                                                       Length 156;
                                                                                                                                                                               Indels
                                                                                                                                                                             0;
                                                                                                                                                                               Gaps
                                                                                                                    95
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156

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В
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                                                                                                                          Qγ
                                                                                                                                                     Matches
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Best Local
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01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                          can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of the multiple tumour suppressor 1 (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1994;
8-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5801236-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             somatic mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW74549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MYRI-) MYRIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of multiple tumour suppressor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1998
156
                       148
                                                96
                                                                         88
                                                                                                   36
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                                                                                                                                                                   Local Similarity
                       D 148
                                           d 156
                                                                                                              ALPNAPNSYGRRPIQVMMMGSARVÄELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-494842/42.
DB; AAV53819.
                                                                                                 alpnapnsygrrpigvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 95
                                                                                                                                                                                                                     156
                                                                                                                                                  81.8%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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94US-0215086.
94US-0215087.
94US-0227369.
94US-0227369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                 63-64; 73pp;
                                                                                                                                                     0;
                                                                                                                                                                Score 121; DB 19; I
; Pred. No. 1.6e-108;
                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                     0
                                                                                                                                                                           Length 156;
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RESULT 15
AAW40524
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                                                                                                                                      Matches 121;
                                                                                                                                               Query Match
Best Local Similarity
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                 (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW40524 standard; Protein;
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                          This sequence represents a human multiple tumour suppression protein, MTS1. The MTS gene locus is also referred to as the familial melanoma
                                                                                                                                                                                                                                                                                                                                               DNA specific for Multiple Tumour Suppressor 1E1-beta gene - useful for the diagnosis of cancers related to MTS1E1-beta
                                                                                                                                                                                                                                                                                                            Disclosure; Column 63-64; 72pp; English.
                                                                                                                                                                                                                                                                                                                                   mutation(s) and their treatment
                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV11238.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-250421/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MTS1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW40524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        (MYRI-)
156 d
                     148 D 148
                                        36 alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv
                                                                                                   28 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
156
                                                                                                                                                                                                                                                                                                                                                                                                                                         MYRIAD
                                                                                                                                                                                             156 AA;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0214582.
94US-0215086.
94US-0215087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0227369.
94US-0251938.
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                                                                                                                                                100.0%;
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                                                                                                                                     0;
                                                                                                                                                Score 121; I
Pred. No. 1
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                                                                                                                                                            DB 19;
                                                                                                                                                .6e-108;
                                                                                                                                     0,
                                                                                                                                                         Length 156;
                                                                                                                                     Indels
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                                                                                                              87
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AAW80524 ID AAW8

AAW80524 standard; Protein; 156

A

RESULT 16

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RESULT 17
AAB1549B
ID AAB154
XX AB154
AC AAB154
XX AB154
XX AB154
XX AB154
XX CABB154
XX CYtost
XX CYtost
XX Cancer
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, predispose towards malignancies such as melanoma, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1995;
07-JUN-1995;
            cancer; gene therapy;
                        Cytostatic; human; multiple tumour suppressor 1; MTS1; diagnostic;
                                                   Human MTS1 protein
                                                                             14-FEB-2001
                                                                                                       AAB15498;
                                                                                                                                AAB15498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              astrocytoma, lymphoma, glioma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Columns 65-66; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A human multiple tumour suppressor 1 (MTS1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                thyroid, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse multiple tumour suppressor gene segment - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW80524;
                                                                                                                                                                                                156 d
                                                                                                                                                                                                                          148 D 148
                                                                                                                                                                                                                                                                                                  96 vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip 155
                                                                                                                                                                                                                                                                           88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-044585/04.
                                                                                                                                                                                                                                                                                                                                                         121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kamb A,
                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA;
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                             (first
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95US-0487033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour suppressor 1 gene; MTS1; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                  uterus
                                                                                                                                Protein;
                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                   81.8%;
            protein replacement therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                and kidneys.
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                                                                                                                                                                                                                                                                                                                                                                    Score 121; DB 20;
Pred. No. 1.6e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             as well as tumours of e.g. the breast
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                Length 156;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer
                                                                                                                                                                                                                                                                                                                                                         0,
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Best Local Similarity 100
Matches 121; Conservative
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human multiple tumour suppressor 1 (MTS1) amino acid sequence. The protein has a cytostatic activity and is used in protein replacement therapy. MTS1 is useful in diagnosing human cancers such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma, cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary, uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is
          Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; p16 protein.
                                                                                                      AAY97524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                uterus, testis, kidney, colon and rectamn. .... .... and protein mimetic useful in gene therapy, protein replacement therapy and protein mimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein composition useful in protein replacement therapy for diagnosing and treating cancer comprises a specific weight percent human multiple tumour suppressor 1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamb
                                                                             15-JAN-2001
                                                                                                                             AAY97524 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Column 63-64; 72pp; English.
                                                  Human p16 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MYRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                156 d
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                                                                                                                                                                                                                                                                             88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                    alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;
                                                                                                                                                                                                                                                    vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-514036/46.
DB; AAA95633.
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                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA;
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94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
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                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                   81.8%;
                                                                                                                                                                                                                                                                                                                                                                   Score 121; DB 21; Pred. No. 1.6e-108;
                                                                                                                                156
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Length 156;
                                                                                                                                                                                                                                                                                                                                                         0
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AAY96053
ID AAYY
XX
AC AAYY
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XX
DT 05-1
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DE Hums
EX
XX
KW Cycl
KW SMOX
KW gene
XX
PN W020
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Best Local :
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08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein or the DNA encoding it are useful for treating neoplasias in animals. T compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays
                                                           Cyclin
smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein and nucleic acid compositions for preventing and tree neoplasias (particularly cancer), comprises a novel chimeric dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2000; 2000WO-US05350
 WO200052159-A1
                                                                                               Human cyclin dependent kinase inhibitor p16
                                                                                                                       05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synchronise cell growth in cultured cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the human pl6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 123; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELL GENESYS INC. (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200052184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                       AAY96053 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                 2000-587315/55.
                                               therapy
                                                           dependent kinase inhibitor; CDKi; INK4; human;
muscle cell; restenosis; vasotropic; antiproli
                                                                                                                                                                                                                                   156
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA90921.
                                                                                                                                                                                                                                                                                                                                                                                                                                            156 AA;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0122974.
99US-0128271.
99US-0128515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ģ
                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gyuris
                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                            Score 121;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mendez MJ,
                                                                                                                                                                                                                                                                                                                                                                                            DB 21; I
1.6e-108;
                                                          K4; human; pl6;
antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finer
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 156;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclin
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein,
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AAY96067
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                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of human p16, a cyclin dependent CC kinase inhibitor (CDKI) that inhibits smooth muscle cell CC proliferation. A claimed method for inhibiting smooth muscle cell coll proliferation involves transducing smooth muscle cells with a CC replication-deficient recombinant adenovirus that lacks a functional CC El region and a functional E4 region, and comprises a transgene CC encoding a CDKI. The CDKI is selected from an INK4 family protein Such as human p16, a CIP/KIP family protein such as p27, active fragments of these, or fusion proteins comprising (active fragments of these, or fusion proteins comprising (active fragments CC and AAY96049). The method is used to inhibit mammalian smooth muscle C cell hyperproliferation induced by injury caused by angioplasty, C stent placement or vein engraftment. It is useful for treating to constitutions of the companion of the cell indicated by angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant lentivirus for inhibiting proliferation of smooth muscle cells in e.g. restenosis, is replication deficient and compr a transgene encoding a cyclin dependent kinase inhibitor
Cyclin dependent kinase inhibitor; CDKi; INK4; human; p16; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000
                                                                       Human cyclin
                                                                                                    05-DEC-2000
                                                                                                                                                               AAY96067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lentiviruses encoding CDKis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CELL-) CELL GENESYS (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2000;
                                                                                                                                                                                                                                      156
                                                                                                                                                                                                                                                                148
                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                          D.
                                                                                                                                                                                                                                                                D 148
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DB; AAA50500.
                                                                                                                                                                                                                                      156
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                             standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US04971.
                                                                       dependent kinase inhibitor pl6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gyuris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENESYS INC
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122974.
99US-0163682.
99US-0457568.
                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finer
                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 121; DB 21;
Pred. No. 1.6e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
 antipsoriatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises
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RESULT
AAY92921
ID AAY
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AC AAY
AC AAY
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XX
XX
DT 11-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ery Match
st Local Similarity
atches 121; Conser
                                                                                                                                                                                                                                                                                                                                          The present sequence is that of human p16, a cyclin dependent kinase inhibitor (CDKi) that inhibits angiogenesis. A claimed method for inhibiting angiogenesis involves transducing an epithelial cell with a transgene encoding (internalizable, secretable) CDKi. The delivery system for the transgene may be a liposome or a recombinant virus. The CDKi is preferably a protein of the CIP/KIP family such as p27, a protein of the INK4 family such as p16, active fragments of these proteins, or a fusion of 2 CDKi proteins such as p27 and p16 (see AAY96068-80). The method is useful in treating conditions associated with angiogenesis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
            11-OCT-2000
                                 AAY52921;
                                                   AAY92921 standard;
                                                                                                                                                                                                                                                                                                    neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy (claimed). Alternatively, the transgene is delivered to an auxiliary cell, and is expressed by that cell sucthat the CDK1 is released into the blood and contacts the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin dependent kinase inhibitor -
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-565501/52.
N-PSDB; AAA50520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 129; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2000WO-US04970
                                                                                                      156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CELL-) CELL GENESYS INC (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200052158-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiproliferative;
                                                                                                                        148 D 148
                                                                                                                                                                               21
                                                                                                                                         96 vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip 155
                                                                                                                                                    88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                      d 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mcarthur J,
                                                                                                                                                                                                                                                                                              cell.
                                                                                                                                                                                                                                                                            156 AA;
                                                                                                                                                                                                                           Conservative
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0122974.
99US-0163682.
99US-0457646.
                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy.
                                                                                                                                                                                                                                   81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gyuris
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                  Score 121; DB 21;
Pred. No. 1.6e-108;
                                                   Ā
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                           Length 156;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                 cell such
                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                  95
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RESULT
AAY91102
ID AAY
XX
AC AAY
XX
DT 12-1
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Best Local Si
Matches 121;
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
AAY91102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to variants (AAA11196-A11206) of the human multiple tumour suppressor 1 (MTS1) protein of which this sequence represents the wild type sequence. The variants have the following changes relative to the wild type coding sequence: A at any of positions 265, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and deletions of nucleotides 290-294, 172-179 or 128-129. The variants are somatic mutations of MST1, indicative of predisposition to melanoma and many other cancers, so detecting them is useful for diagnosis, prognosis and monitoring of cancer (including prenatal analysis). Cells and animals that express the variants are useful as model systems for
                                  AAY91102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic deletions
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mutants of the human multiple tumor suppressor gene, useful as diagnostic markers of cancer, contain specific base alterations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6037462-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;
cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human multiple tumour suppressor 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYRI-)
                                                                                                                           156
                                                                                                                                                             148 D 148
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                                                                                                                                                                                                                                                                                                         28
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                                                                                                                           Ω
                                                                                                                                                                                                                                                                 2000-269915/23
                                                                                                                           156
                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYRIAD GENETICS INC
                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Column 61-62;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0214582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0120130
                                  Protein;
                                                                                                                                                                                                                                                                                                                                                            81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72pp; English.
                                    156
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                            Score 121;
Pred. No.
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                              1.6e-108;
                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                            Length 156;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                           0;
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Вр

156 d 156

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Best Loc
Matches
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8-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                       stomach and used in the
                                                                                                                                                                                                                                                                                                                                                                                                  product is not rully nunchanged in the useful as a model system to study cancer remission and drug treatment which promotes such remission. The present invention relates to somatic mutations and germ line mutations in the MTS gene and their use in the diagnosis and prognosis of human cancer e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a vector (I) comprising an isolated DNA sequence of a multiple tumour suppressor (MTS) gene having a polynucleotide sequence of the human MTSIEI-beta. (I) is useful for introducing wild-type MTS function to a cancerous or pre-cancerous cell which carries diminished or mutant MTS alleles for suppressing neoplastic growth of the recipient cells. (I) is also useful for increasing the level of expression of MTS gene even in tumour cells in which the mutant gene is expressed at a normal level but the gene product is not fully functional. A host cell transformed with (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unuan; multiple tumour suppressor; MTS; somatic mutation; diagnosis; germ line mutation; gene therapy; cytostatic; m leukaemia; astrocytoma; glioblastoma; Lymphoma; glioma; Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        suppressor gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 63-64; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vector useful for gene therapy of cancer associated with mutation in tumor suppressor gene, comprises DNA sequence of multiple tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kamb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2000
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      148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MYRI-) MYRIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6060301-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                   96
                                                                                          88
                                                                                                                                       36
                                                                                                                                                                                   28
                                                                                                                                                                                                                                                  Local
                                         ۵ -
                                                                                                                             2000-349676/30
DB; AAA39353.
                                                                                 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
      148
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                          156 AA;
                                                                                                                                                                                                                                                                                                                                                                                    exemplification
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0480810

97US-0986147

94US-0214582

94US-0215086

94US-0215087

94US-0227369

94US-0251938

95WO-USO3316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0115252
                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents human MTS1, which fication of the present invention.
                                                                                                                                                                                                                                             81.8%;
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                Score 121; DB 21; Pred. No. 1.6e-108;
                                                                                                                                                                                                                                                                                                                                                                                the present
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:2
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                  Length 156;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                        Gaps
                                         155
                                                                                                                                                                                                                        0;
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Q В Qγ DЪ ΩV

В Qy

36 28

ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87 alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv

Query Match Best Local Matches

Similarity

81.8%;

Score 121; DB 21; Pred. No. 1.6e-108; Mismatches

Length 156; Indels

0;

Gaps

0

95

Conservative

0;

Sequence

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AAY59415
XX
XX
AC AAYE
AC AAYE
XX
XX
DE Humm
XX
KW MITS,
KW Lymin
KW Lymin
KW Then
XX
YN US5;
XX
YN
                                                                                              This sequence represents the human MTS1 protein.

CC The invention relates to a method for diagnosing a polymorphism cc associated with a predisposition to cancer by detecting a germ-line cc associated with a predisposition to cancer by detecting a germ-line cc associated with a predisposition to cancer by detecting a gene or its carperssion products in a human sample. The method comprises detecting a cc germ-line alteration of a wild-type MTS gene or its expression products cc in a human sample, the alteration indicating a predisposition to at least cone of the cancers. The cancer is selected from melanoma, leukaemia, cc astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, cc chronic lymphocytic leukaemia (CLL), and cancers of the pancreas, breast, ct thyroid, ovary, uterus, testis, kidney, stomach and rectum. The method cc may be used as the basis for developing very important diagnostic testis capable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is compable of predicting the predisposition to cancer. The MTS gene is considered the many provide in the progression of multiple tumour types and may provide compable of predicting the predisposition to cancer.
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14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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18-MAR-1994;
18-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Column 61-64; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing a polymorphism associated with
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(MYRI-)
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MYRIAD GEN
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94US-0251938.
95WO-US03537.
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94US-0214582
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RESULT :
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AC AAY:
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                This sequence represents the human multiple tumour suppressor 1 (MTS1) protein. The invention relates to the human MTS2 DNA and protein sequences. The DNA sequences are useful for diagnosing or determining a predisposition to cancers e.g. melanoma, leukaemia, lymphoma, glioma, Hodgkin's lymphoma and cancers of the pancreas, breast, thyroid, ovary, bidge, with the pancreas of the pancreas of the pancreas.
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                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                           Multiple tumour suppressor cDNA, useful for diagnosing predisposition to cancer - \,
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N-PSDB; AAZ39974.
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                      VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
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                                                                                                               Conservative
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94US-0251938.
95WO-US03316.
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94US-0215087
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                                                                                                                        81.8%;
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                                                                                                                        Score 121; DB 21; 1; Pred. No. 1.6e-108;
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                                                                                                               Mismatches
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                                                                                                                                   Length 156;
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RESULT :
AAUU21122
ID AAUU4122
ID AAUU4122
AC AAUU
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Best Local S
Matches 121
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17-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the amino acid sequence of human multiple tumour suppressor MTS1. The MTS genes, and expression products, are useful for treating, diagnosing or prognosing human cancer. In particular, the MTS gene is useful for diagnosing a predisposition to or as a gene therapy for melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL), or cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach or rectum. The gene may be used in both cancerous and pre-cancerous cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; multiple tumour suppressor; MTS1; MTS2; therapeutic; cancer; gene therapy; melanoma; leukaemia; astrocytoma; glic lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mouse multiple tumour suppressor gene, useful for diagnosing or prognosing human cancer or as gene therapy for treating cancer, particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of the pancreas or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stone S,
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156
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hes 121;
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Similarity 100.0%;
21; Conservative (
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95WO-US03316.
95US-0487033.
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leukaemia.
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                multiple tumour suppressor (MTS) gene in human cancer. The invention also relates to therapy of human cancer which have a mutation in the MTS gene, including gene therapy, protein replacement therapy, and protein mimetics. The MTS sequences are useful for diagnosing predisposition to human cancer or for diagnosing and prognosing human cancers such as melanoma, leukaemia, astrocytoma, glioblastoma human cancers such as melanoma, leukaemia, astrocytoma, glioblastoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma;
glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;
pancreas; breast; thyroid; ovary; uterus; testis; kidney; stomach;
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N-PSDB; AAD04692, AAD04693, AAD04694, AAD04724,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human multiple tumour suppressor 1 (MTS1) protein
                                                                                                                                                                                                              The present sequence is chromosome 9p21.
                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Column 63-64; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         prognosis
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel multiple tumor suppressor proteins useful for diagnosis and prognosis of human cancer and for screening drugs for cancer trea
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                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                       ymphoma, glioma, Hodgkin's lymphoma, CfL and cancers of pancreas, reasts, thyroid, owary, uterus, testis, kidney, stomach and rectum. They are also used for screening drugs for cancer treatment. They are also used for screening they are also used for screening drugs for cancer treatment.
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90
                                                     ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip 155
                            VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple tumour suppressor; MTS1; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYRIAD
                                                                                                                            Similarity
                                                                                                                                                                                    156
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0486047.
94US-0214582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0120131.
                                                                                                                           81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC
                                                                                                              0;
                                                                                                                            Score 121;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                Mismatches
                                                                                                                                           DB 22;
                                                                                                                           .6e-108;
                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD04727,
                                                                                                                                        Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                            for cancer treatment
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        somatic mutation;
a astrocytoma; CLL;
                                                                                                                                                                                                                                                                                    glioblastoma,
                                                                                                                                                                                                                                                                                                                                                                      in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD04734,
                                                                                                                0,
                                                                                                              Gaps
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RESULT 2
AAB36890
ID AAB3
                                                                                                                                                                                             RESULT AAB67334
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                                                                             В
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                                                                                                                                                           Query Match
Best Local
                                                                                                                                                  Matches 121;
                                                                                                                                                                                                                                                                                                                                                                         18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
01-JUN-1994;
                                                                                                                                                                                                                     The present invention relates to human multiple tumor suppressor-2 (MTS2) gene. The invention is useful for diagnosing, prognosing and treating cancers. It is also useful for screening drugs for cancer
                                                                                                                                                                                                                                                                        Novel multiple tumor suppressor gene useful for diagnosing, prognosing and treating cancers, such as melanoma, leukemia, glioblastoma and Hodgkin's lymphoma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; multiple tumour suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by multiple tumour suppressor open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB67334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB67334 standard;
AAB36890 standard; Protein; 156 AA.
                                                                                                                                                                                                                                                                                                             WPI; 2001-158668/16
                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6180776-B1
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                             therapy and gene therapy.
                                                                                                                                                                                                                                                         Disclosure; Column 63; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
                                                                                                                                                                                                                                                                                                                                               (MYRI-) MYRIAD
                                                                                                                                                                                                                                                                                                                                                                 17-MAR-1995;
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                                                            148 D 148
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                                                                                                             sapiens
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                                                                                                                                                           Similarity
                                                                                                                                                                                             156 AA;
                                                                                                                                                 Conservative
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94US-0214582.
94US-0215086.
94US-0215087.
94US-0251938.
95WO-US03316.
                                                                                                                                                                                                                                                                                                                                               GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0120129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                          81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
                                                                                                                                                  0;
                                                                                                                                                          Score 121; DB 22; 1
Pred. No. 1.6e-108;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTS; cancer; gene therapy
                                                                                                                                                    0
                                                                                                                                                                  Length 156;
                                                                                                                                                    Indels
                                                                                                                                                   0;
                                                                                                                                                  Gaps
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RESULT
AAY975;
ID AJ
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AC AJ
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                               hery Match
                                                                                                                                                                                                specifically binds to a human multiple tumour suppressor (MTS). The invention is useful for detecting differences in the absence of MTS peptides, to screen a tissue or to detect mutant MTS gene products. The antibodies will immunoprecipitate MTS proteins from solution as well as react with MTS protein on Western or immunoblots of polyacrylamide gels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTS;
                                                                                                                                                                                                                                                                     New multiple tumor suppressor 2-specific antibodies useful for detecting differences in the absence of the peptides or mutant products, or for screening tissues \dot{}
                                                                                                                                                                                                                                                                                                                      Kamb
                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Multiple Tumour Suppressor 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36890
                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-1998;
                                                                                                                                                                                                                                                        Claim 1;
  15-JAN-2@01
               AAY97522;
                            AAY97522
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                           The present invention relates to an antibody or its fragment
                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                   (MYRI-)
                                                                             148
                                                               156 d
                                                                                                                                                       Local
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                                                                                          vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
                                                                                                                    2001-014867/02.

)B; AAC83071.
                                                                             U
                                                                                                  VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP
                                                                                                                                                  121;
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                                                                156
                                                                                                                                                                                                                                                                                                                                    MYRIAD
                                                                                                                                                  h 81.8%;
Similarity 100.0%;
21; Conservative (
                                                                                                                                                                                                                                                          Column
                             standard;
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94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
                                                                                                                                                                                    ĀΑ;
                                                                                                                                                                                                                                                                                                                                     GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                    95US-0486047
94US-0214582
                                                                                                                                                                                                                                                          63;
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                             Protein;
                                                                                                                                                                                                                                                        71pp;
  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suppressor; cancer; antibody.
                                                                                                                                                                                                                                                         English.
                              228
                                                                                                                                                  0;
                                                                                                                                                        Score 121;
Pred. No.
                                                                                                                                                  Mismatches
                                                                                                                                                          1.6e-108;
                                                                                                                                                   0
                                                                                                                                                                Length 156;
                                                                                                                                                   Indels
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Query Match
Best Local S
Matches 121
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08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the human W9 protein.
The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDK1) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to synchronise cell growth in cultured cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; W9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2000; 2000WO-US05350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200052184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Cyclin dependent
                           Antiproliferative truncated p27-p16 fusion protein
                                                                 05-DEC-2000
                                                                                               AAY96051
                                                                                                                                  AAY96051 standard; Protein;
                                                                                                                                                                                                                                                 148
                                                                                                                                                                                                                                                                                  168
                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                 88
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DB; AAA90919.
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                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL GENESYS INC MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McArthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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99US-0128271.
99US-0128515.
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   kinase inhibitor;
                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gyuris
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 21; Pred. No. 2.2e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ļ
                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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   CDKi; CIP; KIP; p27; INK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
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                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                     dependent kinase inhibitor (CDKI) domain is retained, and human place protein (see AAY96053), with no (GJy4Ser)3 hinge. A claimed method CC for inhibiting smooth muscle cell hyperproliferation involves CC transducing smooth muscle cells with a replication-deficient CC comprises a transgene encoding a CDKI. The CDKI is selected from CC an INK4 family protein such as human pl6, a CIP/KIP family protein CC comprising (active fragments of these, or fusion protein and a CC CIP/KIP family protein (see AAY96046 and AAY96049). A fusion protein comprising W9 is specifically claimed. The method is used to inhibit mammalian smooth muscle cell hyperproliferation induced CC by injury caused by angioplasty, stent placement or vein CC centraftment. It is useful for treating vascular pathologies e.g., CC CIP/KIP ife and to elaimed are recombinant lentiviruses encoding CC CDKis. Use of truncated p27 was designed to increase the protein's CC in the negative regulation of CDKi activity. The p27-p16 fusion CC CDKIS interact with the CDK4/cyclinA and conversion at
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                   multiple points.
                                                                                                                                                                                                                                                                                                                                                                        proteins interact with CDK2/cyclinE complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of W9 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 118-119; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant lentivirus for inhibiting proliferation of smooth muscle cells in e.g. restenosis, is replication deficient and comprises a transgene encoding a cyclin dependent kinase inhibitor \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p16; human;
vasotropic;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            truncated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELL GENESYS INC (MITO-) MITOTIX INC.
                                                                           108
                         88
                                                                                                                         28
                         VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                  ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
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                                                                        alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv
Similarity
                                                                                                                                                                                                                                                                                                  228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        smooth muscle cell; hyperproliferation; restenosis;
antiproliferative; gene therapy; mutant; mutein.
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gyuris J,
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99US-0163682.
99US-0457568.
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1..71
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84..228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein (see AAY96048)
                                                                                                                                                                                                  81.8%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                        and inhibit cell cycle progression at
                                                                                                                                                                           0
                                                                                                                                                                                             Score 121; DB 21;
Pred. No. 2.2e-108;
                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in which only the
                                                                                                                                                                           0;
                                                                                                                                                                                                                         Length 228;
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cyclin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
            The present sequence is that of fusion protein W9 comprising an XY -terminal truncated human p27 protein (see AAY96075) in which only Ct the cell dependent kinase inhibitory (CDKi) domain was retained, and a human p16 protein (see AAY9607). This version of W9 differs from that of AAY96076 by the lack of a hæmag9lutinin tag. A C claimed method for inhibiting angiogenesis involves transducing an CC epithelial cell with a transgene encoding a CDKi. The transgene conclusion of the CIP/KIP family such as p27, a protein of the CIP/KIP family such as p27, a protein of the CIP/KIP family such as p27, a protein comprising 2 C CINK4 family such as p16, active fragments of these (e.g. amino acids C 5-93 or 12-178 of human p27), or a fusion protein comprising 2 C CDKi proteins such as (truncated) p27 and p16 (see AAY96068-80). A C method is used to treat conditions associated with angiogenesis, method is used to treat conditions associated with angiogenesis, constitutions the comprision of the contraction of the conditions associated with angiogenesis and constitutions associated with angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                  Inhibiting angiogenesis and treating angiogenesis associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
endometriosis; psoriasis; vascular retinopathy; cytostatic;
antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000WO-US04970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiproliferative; gene therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclin dependent kinase inhibitor; CDKi; CIP; KIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96078
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   vascular retinopathy
                                                                                                                                                                                                                                                                                                                      dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA50533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELL-) CELL GENESYS INC. (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                     Example 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mcarthur J,
                                                                                                                                                                                                                                                                                   Page 126-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibitor p27(25-93)-p16 fusion
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99US-0163682.
99US-0457646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= p27(25-93)
84..228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= p16
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   (claimed).
                                                                                                                                                                                                                                                                                     138pp; English.
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RESULT 3
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Best Local
The invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing a least one CDK-binding motif for binding and inhibiting activity of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graff;
                                                                                                                                                                                                                                                           Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancer.
                                                                                                                                                                                     Claim 63; Page
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tachycardia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Truncated p27/p16 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW95105 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               delivered to an auxiliary cell, and is expressed by that cell such that the CDKi is released into the blood and contacts the target epithelial cell. Use of truncated p27 was designed to increase the protein's half-life and to eliminate potential phosphorylation sites involved in the negative regulation of CDKi activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                          1999-153770/13.
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                                                                                                                                                                                                                                                                                                                                                                                AAX26233
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                                                                                                                                                                                                                                       neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                            85; 88pp; English.
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Pred. No. 2.2e-108;
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                                                                                                                                                                                                                                                              vascular injury, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         periodontal; spermatogenesis;
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                                      containing at
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Best Local
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08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See AAX26220 for detailed uses of the recombinant transfection system. The present sequence represents a human truncated p27/pl6 fusion protein.
                                                          Protein and nucleic acid compositions for preventing and tree neoplasias (particularly cancer), comprises a novel chimeric dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                       Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; W9 protein.
                                                                                                                                                                            (CELL-) CELL GENESYS (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                     01-MAR-2000;
                                                                                                                                                                                                                                                                                               08-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                               Human
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                                                                                                              2000-587315/55
DB; AAA90931.
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                                                                                                                                                                                                                                                                                                                                                sapiens.
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                                                                                                                                                     McArthur J,
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99US-0128271.
99US-0128515.
                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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Pred. No.
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2.3e-108;
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This sequence The invention

represents the human W9 protein. relates to a protein composition comprising a novel

Example 1; Page 119; 126pp;

English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 121
                                                                                                                                                                                                                                                                                                             01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified chimeric cyclin dependent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to synchronise cell growth in cultured cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4; p16; human; smooth muscle cell; hyperproliferation; restenosi vasotropic; antiproliferative; gene therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96049 standard;
  Novel recombinant lentivirus for muscle cells in e.g. restenosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antiproliferative truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96049
                                                                                       N-PSDB; AAA50496
                                                                                                                                                                                                                               (CELL-) CELL GENESYS INC (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000WO-US04971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200052159-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpnapnsygrrpiqvmmmgsarvaelllihgaepncadpatltrpvhdaaregfldtlv 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                                                                 2000-594183/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                        Gyuris
                                                                                                                                                                                                                                                                                                             99US-0122974.
99US-0163682.
99US-0457568.
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12..80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                           Finer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p27-p16 fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA
  inhibiting proliferation of smooth
is replication deficient and comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restenosis;
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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a transgene encoding a cyclin dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple
                                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                   angiogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antirheumatic; gynaecological; antipsoriatic; antirheumatic; gynaecological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                               Protein
                                                                            Key
                                                                                                                                                       antiproliferative;
                                                                                                                                                                                                                     Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p27;
                                                                                                                                                                                                                                               Angiogenesis inhibitor p27(25-93)-p16 fusion
                                                                                                                                                                                                                                                                                   05-DEC-2000
                                                                                                                                                                                                                                                                                                                    AAY96076;
                                                                                                                                                                                                                                                                                                                                                AAY96076 standard; Protein;
Protein
                                                            Peptide
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 /label= p27(25-93)
94..237
                                12..80
                                                                           Location/Qualifiers
                                             /label= Haemagglutinin_epitope
                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
100.0%;
                                                                                                                                                         therapy;
                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 121;
Pred. No.
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                                                                                                                                                         mutant;
                                                                                                                                                           mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3e-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                CC N-terminal haemagglutinin tag, a truncated human p27 protein (see CAY96075) in which only the cell dependent kinase inhibitory domain CC was retained, and a human p16 protein (see AAY96067). A claimed method CC for inhibiting angiogenesis involves transducing an epithelial cell with a transgene encoding a cyclin dependent kinase inhibitor (CDKi). CC The delivery system is a liposome or a recombinant virus. The CDKi CC is a protein of the CIP/KIP family such as p27, a protein of the CZ (CINA) family such as p16, active fragments of these (e.g. amino acids C2 5-93 or 12-178 of human p27), or a fusion protein comprising 2 CC (DKi proteins such as (truncated) p27 and p16 (see AAY96068-80). A CC method in which the CDKi is w9 is specifically claimed. The CC method is used to treat conditions associated with angiogenesis, CC e.g. neoplassia, rheumatoid arthritis, endometriosis, psoriasis and CC vascular retinopathy (claimed). Alternatively, the transgene is CC delivered to an auxiliary cell, and is expressed by that cell such CC that the CDKi is released into the blood and contacts the target CC epithelial cell. Use of truncated p27 was designed to increase the CCC involved in the negative regulation of CDKi activity.
                                                                                                                                                            Query Match
Best Local
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting anglogenesis and treating anglogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelia. cell with a recombinant virus having a transgene encoding a cyclin dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 123-124; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELL-) CELL GENESYS INC. (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000;
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        177
                                                                         117
                                       88
                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is that of fusion protein W9 comprising
ALPNAPNSYGRRPIQYMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                    alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-565501/52.
                                                                                                                                             121;
                                                                                                                                                          Similarity
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                                                                                                                                            Conservative
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99US-0457646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0122974
                                                                                                                                                      81.8%; Score 121; DB 21; 100.0%; Pred. No. 2.3e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gyuris
                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                          Mismatches
                                                                                                                                                                        Length
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A claimed method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial
                                                                                                                                        0;
                                                                                                                                      Gaps
                                                                                                      87
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RESULT 3
AAW95106
ID AAW9
XX
AC AAW9

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AAW95106 standard; Protein;

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AAW95106;

P Q

148 237

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237

D 148

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                                                                                                                                                                                                                                                                                         CC (CDKs), particularly CDK/cyclin comprises: (1) first gene construct
CC transfection system (A) that comprises: (1) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC comprising a sequence encoding and inhibiting activity of a
CC (EX, linked to a transcription regulator functional in eukaryotic cells;
CC (ii) second gene construct comprising a sequence encoding a polypeptide
CC that promotes endothelialisation, and (iii) a gene delivery composition
CC for delivering the GCs to a cell for transfection. Also provided are
CC nucleic acids encoding a fusion protein (FP) containing: (i) a
CC therapeutic polypeptide sequence (TP) from an intracellular protein that
CC alters a cellular process when FP enters the cell, and (ii) a
CC transcellular polypeptide sequence (TP) that promotes transcytosis of
CC encosists of at least one CDK-binding motif and a TCP. See
CC AAX26220 for detailed uses of the recombinant transfection system. The
CC present sequence represents a human truncated p27/p16 fusion protein.
                                                                                                                                                                                                        Matches 121;
                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel inhibitors of cyclin-dependent kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 63; Page 85; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrosis and neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhil CDK-binding motif; endothelialisation; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Truncated p27/p16 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1999 (first entry)
252 d
                                148 D
                                                                  192
                                                                                                                                     132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracellular;
                                                                                                 88
                                                                                                                                                                     28
                                                                                                                                                                                                                        Local Similarity
                                                                                                                                VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-153770/13.
DB; AAX26234.
                                                               vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
                                148
252
                                                                                                                                                                                                                                                                                           252
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcellular; transcytosis; vascular wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0902572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US15759
                                                                                                                                                                                                                    81.8%;
                                                                                                                                                                                                      0;
                                                                                                                                                                                                                    Score 121; DB 20;
Pred. No. 2.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŗ,
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                    Length 252;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapeuti
                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restenosis;
eutic; acne;
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hair;
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AAY96050
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                                                                                                                                                                                     20
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                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1999;
08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                 This sequence represents the human W10 protein. The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to synchronise cell growth in cultured cells.
AAY96050 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclin dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chimeric cyclin
adenovirus E4 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY97535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY97535 standard; Protein; 252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 120; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200052184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human W10 protein sequence
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CELL-) CELL GENESYS INC (MITO-) MITOTIX INC.
                                                              252
                                                                                       148
                                                                                                                192
                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-MAR-2000;
                                                                                                                                       88
                         38
                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                              Q,
                                                                                     D 148
                                                                                                                       VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                          ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-587315/55
                                                                                                           {\tt vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip}
                                                                                                                                                             alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 191
                                                              252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA90932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McArthur J,
                                                                                                                                                                                                                                                                            252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US05350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122974.
99US-0128271.
99US-0128515.
                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                       81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dependent kinase inhibitor;
neoplasia; W10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gyuris J,
252 AA
                                                                                                                                                                                                               0;
                                                                                                                                                                                                                          Score 121; DB 21; Pred. No. 2.5e-108;
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendez MJ,
                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Finer
                                                                                                                                                                                                                                     Length 252;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDKi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy;
                                                                                                                                                                                                              0,
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       87
                                                                                                                                                                                                              0;
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cc claimed, a (1945er) 3 hinge, and human p16 protein (see AAY96053). A cc claimed method for inhibiting smooth muscle cell hyperproliferation convicus transducing smooth muscle cells with a replication-deficient recombinant adenovirus that lacks functional E1 and E4 regions, and comprises a transgene encoding a CDK1. The CDK1 is selected from the comprises a transgene encoding a CDK1. The CDK1 is selected from the comprise of the comprise of the comprise of the comprising (active fragments of these, or fusion protein and a CIPKIP family protein (see AAY96046 and AAY96049). The method is used to inhibit mammalian smooth muscle cell hyperproliferation induced by injury caused by angioplasty, stent placement or vein the surface of truncated p27 was designed to increase the protein's comprise of truncated p27 was designed to increase the protein's chalf-life and to eliminate potential phosphorylation sites involved in the negative regulation of CDK1 activity. The p27-p16 fusion control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclin depen p16; human; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel recombinant lentivirus for inhibiting proliferation of muscle cells in e.g. restenosis, is replication deficient and a transgene encoding a cyclin dependent kinase inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of W10 fusion protein comprising a haemagglutinin tag, a truncated human p27 protein (see AAY96048) in which only the cyclin dependent kinase inhibitor (CDKi) domain is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                        multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 116-117; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200052159-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiproliferative truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELL GENESY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-594183/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4; uman; smooth muscle cell; hyperproliferation; restenosiopic; antiproliferative; gene therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA50497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL GENESYS INC
                                        points.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US04971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122974.
99US-0163682.
99US-0457568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= p27(12-178)
81..95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= p16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Haemagglutinin_epitope
12..80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p27-p16 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and comprises
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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 121;
                                                                                                                                                      01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                       angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
endometriosis; psoriasis; vascular retinopathy; cytostatic;
antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                          Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY96077 standard; Protein;
                                                                                                                                                                                                             08-SEP-2000
                                                                                                                                                                                                                              WO200052158-A1
                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                  Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96077;
                  Example 1; Page 124-125; 138pp;
                                     dependent kinase
                                                                                 N-PSDB; AAA50532.
                                                                                          WPI; 2000-565501/52
                                                                                                            Patel S,
                                                                                                                             (CELL-)
                                                                                                                                                                                           28-FEB-2000; 2000WO-US04970
                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                antiproliferative; gene therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitor p27(25-93)-p16 fusion W10
                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-2000
                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 d 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 D 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 ALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv
                                                                                                                             MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                           Mcarthur J,
 sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                       99US-0122974.
99US-0163682.
99US-0457646.
                                                                                                                                                                                                                                                                          /label= p27(12-178)
81..95
                                                                                                                                                                                                                                                          /label= Hinge
108..252
                                                                                                                                                                                                                                                                                             /label= Haemagglutinin_epitope
12..80
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                     inhibitor
                                                                                                                                                                                                                                               /label= p16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
                                                                                                           Gyuris
that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 121;
Pred. No.
                                                                                                            Ų.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
fusion protein W10 comprising an
                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
2.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                         AAY96079
  밁
                                                                                                                                                                                                                                                                                                                                     QΥ
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                                                                                                                                                                                                                                                                                                                                                                        Qy
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                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                           RESULT
                                                                                                кеу
                                                                                                                             Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
          28-FEB-2000; 2000WO-US04970
                            08-SEP-2000.
                                                                        Protein
                                                                                          Protein
                                                                                                                   Synthetic
                                                                                                                                                       mutein.
                                                                                                                                                                                                                                                         AAY96079;
                                                                                                                                                                                                                                                                                                                                       148 D 148
                                                                                                                                                                                                                                                                                                                     252 d 252
                                                                                                                                                                                                                                                                                                                                                                          88
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CC N-terminal haemagglutinin tag, a truncated human p27 protein (see AAY96075) in which only the cyclin dependent kinase inhibotry domain CC is retained, a (Gly4Ser)3 hinge, and human p16 protein (see AAY96067). CC A claimed method for inhibiting angiogenesis involves transducing an CC epithelial cell with a transgene encoding a cyclin dependent kinase cc inhibitor (CDKi). The delivery system is a liposome or a recombinant CC virus. The CDKi is a protein of the CIP/KIP family such as p27, a CC protein of the INK4 family such as p16, active fragments of these CC (e.g. amino acids 25-93 or 12-178 of human p27), or a fusion protein CC comprising 2 CDKi proteins such as (truncated) p27 and p16 (see CC AAY96068-80). The method is used to treat conditions associated with CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis, CC psoriasis and vascular retinopathy (claimed). Alternatively, the CC transgene is delivered to an auxiliary cell, and is expressed by CC transgene is delivered to an auxiliary cell, and is expressed by CC confacts the target epithelial cell. Use of truncated p27 was CC designed to increase the protein's half-life and to eliminate CC potential phosphorylation sites involved in the negative CC regulation of CDKi activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                              Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; human; p; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-2000 (first entry)
WO200052158-A1
                                                                                                                                                                                                                                                                                                                                                    antiproliferative; gene therapy; HIV; protein secretion; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secretable angiogenesis inhibitor p27(25-93)-p16 fusion W9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY96079 standard; Protein; 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 alpnapnsygrrpigvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                      Location/Qualifiers 97..166
                                                                                                                                                                                                                                                sapiens.
n immunodeficiency virus
                                                                                 /label= p27(25-93)
180..323
                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
                                                       p16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121; DB 21;
Pred. No. 2.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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AAW95103
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                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See AAY96075) in which only the cyclin dependent kinase inhibitor (CDKi) domain is retained, and the human p16 protein (see AAY96067).

A claimed method for inhibiting angiogenesis involves transducing an epithelial cell with a transgene encoding a CDKi. The delivery system is a liposome or a recombinant virus. The CDKi is a protein of the CIP/KIP family such as p27, a protein of the CIP/KIP family such as p27, a protein of the CIP/KIP family such as p27, a protein of the CIP/KIP family such as p27, a protein of the comprising 2 CDKi proteins such as (truncated) p27 and p16 (see CAAY96068-80). A method in which the CDKi is w9 is specifically claimed. The method is used to treat conditions associated with angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy (claimed). Alternatively, the transgene is delivered to an auxiliary cell, and is expressed by that cell such that the CDKi is released into the blood and contacts the target epithelial cell. Use of truncated p27 was designed to increase the protein's half-life and to eliminate protein a contential phosphorylation sites involved in the negative
                                                                                                                                                                                                                                                                                                                                                                                                                             tches
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05-NOV-1999;
09-DEC-1999;
Truncated p27/p16 fusion protein
                                25-MAY-1999 (first entry)
                                                                           AAW95103;
                                                                                                        AAW95103 standard; Protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of cyclin dependent kinase inhibitor (CDKi) w9. This version of w9 differs from that of AAY96076 by the inclusion of the proinsulin leader sequence and a translocation sequence from HIV tat amino acids 1-72. w9 (see AAY96076) comprises a truncated human p27 protests.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin with a recombinant virus having a transgene encoding a cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation of CDKi activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 130-131; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA50534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is that of a secretable,
                                                                                                                                                                                                                                                                                                                                                                 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
                                                                                                                                                                                                      ۵
                                                                                                                                                                                                                                         D 148
                                                                                                                                                                                                                                                                      vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip 322
                                                                                                                                                                                                                                                                                          VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                              alpnapnsygrrpigvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 262
                                                                                                                                                                                                                                                                                                                                                                                                                               121;
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                                                                                                                                                                                                      323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0122974.
99US-0163682.
99US-0457646.
                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 121; DB 21; 100.0%; Pred. No. 3.1e-108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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AAY97532
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                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells: (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cicl, and (iii) a gene delivery composition concleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See present sequence represents a buman transcated 277716 fixed a containing that the combinant transfection system. The
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
AAY97532 standard; Protein; 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion and chimaeric proteins including cyclin-dependent kinase binding motif used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX26220 for detailed uses of the recombinant transfection system. 1 present sequence represents a human truncated p27/p16 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 63; Page 83; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09906540-A2
                                                                                                334 d
                                                                                                                                                                    fibrosis and neurodegeneration
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                                                                                                                                       148 D 148
                                                                                                                                                                                                                                                   214 alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 273
                                                                                                                                                                                                                                                                         28 ALPNAPNSYGRRPTQVMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                                                                                                                                                                                                                                                                                     121;
                                                                                                                                                                                                                                                                                                                                                                                                                                      334 AA;
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                      81.8%;
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Pred. No.
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RESULT 43
AAY96047
ID AAY,960
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AC AAY960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uery Match
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08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; W8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cycl dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200052184-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDKi) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel S,
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     05-DEC-2/000
                                                        AAY96047;
                                                                                                           AAY,96047 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synchronise cell growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human W8 protein.
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                                                                                                                                                                                                                                                                                                                                      Local
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DB; AAA90929.
                                                                                                                                                                                                                                                                                                                                                                                            VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                      334
                                                                                                                                                                                                                                                                                      148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 117-118; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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  (first entry)
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99US-0128271.
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                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
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Novel recombinant lentivirus for inhibiting proliferation of smooth muscle cells in e.g. restenosis, is replication deficient and compra a transgene encoding a cyclin dependent kinase inhibitor \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4 p16; human; smooth muscle cell; hyperproliferation; restenos vasotropic; antiproliferative; gene therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1999;
05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiproliferative truncated p27-p16 fusion protein
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-1999;
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                          cell cycle
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                         progression at multiple points
 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0122974.
99US-0163682.
99US-0457568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= p27(12-178)
177..334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Haemagglutinin_epitope
12..176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p16
                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₩8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restenosis;
                                                                                                                                                                                                                                                                                                                                                                                               comprises
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Query Match
Best Local Similarity
Matches 121; Conser

Conservative

0,:

Score 121; DB 21; Pred. No. 3.2e-108; 0; Mismatches 0;

Length 334; Indels

0

Gaps

0

81.8%;

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RESULT
AAY96074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                       01-MAR-1999;
05-NOV-1999;
09-DEC-1999;
N-terminal haemagglutinin tag, a truncated human p27 protein (see AAY96072) in which the first 12 N-terminal and the final 21 C-terminal amino acids of full-length p27 (see AAY96066) are deleted, and a C-terminal human p16 protein (see AAY96067). A claimed method for inhibiting angiogenesis involves transducing an epithelial cell with a transgene encoding a cyclin dependent kinase inhibitor (CDKi). The delivery system is a liposome or a recombinant virus. The CDKi
                                                                              The
                                                                                                                                                                                                                                      (CELL-)
                                                                                                   Example 1; Page 120-122;
                                                                                                                        Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endot cell with a recombinant virus having a transgene encoding a dependent kinase inhibitor
                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                 Patel S,
                                                                                                                                                                                                                                                                                                                    28-FEB-2000; 2000WO-US04970
                                                                                                                                                                                                                                                                                                                                                                WO200052158-A1
                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endometriosis; psoriasis; vascular retinopathy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis; inhibitor; neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclin dependent kinase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96074 standard; Protein; 334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitor p27(12-178)-p16 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 d 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                             present sequence is that of fusion protein W8 comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D 148
                                                                                                                                                                                            2000-565501/52
                                                                                                                                                                                                                                      CELL GENESYS MITOTIX INC.
                                                                                                                                                                               AAA50529
                                                                                                                                                                                                                Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                       99US-0122974.
99US-0163682.
99US-0457646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; gynaecological; ar
ive; gene therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                  /label= p27(12-178)
177..334
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Haemagglutinin_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   /label= p16
                                                                                                                                                                                                                                                   INC
                                                                                                                                                                                                                Gyuris
                                                                                                  138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDKi; CIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antipsoriatic;
                                                                                                                                   an endothelial
oding a cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273
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RESULT 45
AAW23536
ID AAW235
XX
AC AAW235
XX
DT 16-MAJ
XX
DE CDK 1
XX
COLUMN
KW FUSIC
KW COLUMN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is a protein of the CIP/KIP family such as p27, a protein of the INK4 family such as p16, active fragments of these (e.g. amino acids 25-93 or 12-178 of human p27), or a fusion protein comprising 2 CDKi proteins such as (truncated) p27 and p16 (see AAY96068-80). The method is used to treat conditions associated with angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy (claimed). Alternatively, the transgene is delivered to an auxiliary cell, and is expressed by that cell such that the CDK1 is released into the blood and contacts the target epithelial cell. Use of truncated p27 was designed to increase the protein's half-life and to eliminate potential phosphorylation sites involved in the negative regulation of CDK1 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene; chimeric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder;
                                                                                      Claim 40; Page 46-48; 58pp; English
                                                                                                                                             diseases
                                                                                                                                                                       Chimeric inhibitor of
therapy of cancer and
                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09727297-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue degeneration; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDK inhibitory fusion protein pl6p27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW23536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23536 standard;
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                                                                                                                                                                                                                                                                                                                                                                                               (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1997-393685/36.
DB; AAT74053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip 333
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                                                                                                                                                                                                                                                                                                                                        Gyuris J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0589981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US00569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                        Lamphere
                                                                                                                                                                       cyclin dependent kinase - other proliferative and d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 121; DB 21;
Pred. No. 3.2e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches

    useful for gene
differentiative

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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This sequence derived from a

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represents a fusion of

the

human

polypeptide p27 and p16 o

of the invention.

It was

chimeric

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AAW95107
BXBXBXB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) cc binding motifs from at least two different proteins that bind to CDKs. CC Particularly they inhibit cell-cycle progression. They can be used to cc treat a wide range of proliferative disorders, e.g. cancer, leukaemia, cc psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or they cc degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's cc diseases, gastric ulcers and autonomous diseases of the peripheral cc nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculatis, and to inhibit spermatogenesis or cogenesis. The chimeric proteins can also be used in vitro to maintain cc cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK/Cyclin complex than binding motifs used individually (since they may bind to CDK involved in different stages of the CBH cycle.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                   Нопо
                                                                                                                                                                                                                                                                                                           Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
N-PSDB; AAX26235
               WPI; 1999-153770/13
                                               Beach DH,
                                                                              (MITO-) MITOTIX INC
                                                                                                                 29-JUL-1997;
                                                                                                                                                 29-JUL-1998;
                                                                                                                                                                                  11-FEB-1999
                                                                                                                                                                                                                  WO9906540-A2
                                                                                                                                                                                                                                                                                    tachycardia;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human p16p27 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95107 standard; Protein; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 d 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 D 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                    inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cycle).
                                             Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                   ammation; neurodegeneration; human; p27; p16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                 97US-0902572
                                                                                                                                                 98WO-US15759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%; Score 121; DB 18; 100.0%; Pred. No. 3.5e-108;
                                               Lamphere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                           apeutic; acne;
  repair; hair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See AXX26220 for detailed uses of the recombinant transfection system. The
                                                                                                                                                                                          WO9906540-A2
                                                                                                                                                                                                                                                                                                                                                      CDK-binding motif; endothelialisation; fusion protein; therapeutic; intracellular; transcellular; transcytosis; vascular wound; repair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; cellular proliferation; rheumatoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel inhibitors of cyclin-dependent kinase (CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                             29-JUL-1998;
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human p16p27 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW95096 standard; Protein; 365 AA
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                                                                                                                                    11-FEB-1999
                                                                                                                                                                                                                                                                                                     tachycardia;
                                                                                                                                                                                                                                                                                                                               tumour;
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                                                                                                                                                                                                                                                                                                                            inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                             98WO-US15759
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                                                                                                                                                                                                                                                                                                                               periodontal;
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97US-0902572

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CCKs), particularly CDK/cyclin complexes. It provides a recombinant CC transfection system (A) that comprises: (i) first gene construct CC comprising a sequence encoding an inhibitory polypeptide containing at CCC comprising a sequence encoding an inhibitory polypeptide containing at CCC CDK. linked to a transcription regulator functional in eukaryotic cells; CCC ii) second gene construct comprising a sequence encoding a polypeptide CCC that promotes endothelialisation, and (iii) a gene delivery composition CCC for delivering the GCs to a cell for transfection. Also provided are CCC uncleic acids encoding a fusion protein (FP) containing: (i) a CCC therapeutic polypeptide sequence (PP) from an intracellular protein that CCC transcellular process when FP enters the cell, and (ii) a CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of the recombinant transfection system. The CCC transcellular polypeptide sequence (TCC) that promotes transcytosis of the recombinant transfection system.
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Best Local
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   01-MAR-1999;
                                                                 01-MAR-2000;
                                                                                                                                                                                                        WO200052184-A1
                                                                                                                                                                                                                                                                                                                                               Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; W4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human W4 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY97527;
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   99US-0122974
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100.0%; Pr
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3.5e-108;
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RESULT 4
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Best Local Similarity
                                                        01-MAR-1999;
08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to synchronise cell growth in cultured cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclin dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                        Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; W6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human W6 protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 121; DB 21; ilarity 100.0%; Pred. No. 3.5e-108; Conservative 0; Mismatches 0;
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                                                        99US-0122974.
99US-0128271.
99US-0128515.
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99US-0128515.
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(CELL-) CELL GENESYS INC

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                                Misc-difference
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                                                                                                                            Key
Peptide
                                                                                                                                                              Homo sapiens
Synthetic.
                                                                                                                                                                                            Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4; p16; human; smooth muscle cell; hyperproliferation; restenosis; vasotropic; antiproliferative; gene therapy.
                                                                                                                                                                                                                                                                   05-DEC-2000
                                                                                                                                                                                                                                                                                          AAY96042;
                                                                                                                                                                                                                                                                                                                AAY96042 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human W6 protein. The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to synchronise cell growth in cultured cells.
                                                                                                                                                                                                                                            Antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclin dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 113-114; 126pp;
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21; Conservative
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                                  /note=
149
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                                                                               /label= p27
212..365
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                                                                'label= p16
                                                                                                                'label= Haemagglutinin_tag
                                                                                                                                                                                                                                            p27-p16 fusion protein W4.
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                      "encoded by GAG"
                                             "encoded
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                                                                                                                                                                                                                                                                                                                                                                         Search completed: September 19, Job time: 245 sec
                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of p27-p16 fusion protein W4 comprising CC an N-terminal haemagilutinin tag, the human p27 protein (see AAY96052), CC and the human p16 protein (see AAY96053), with no (G194Ser)3 hinge. CC It is encoded by a nucleic acid obtained by PCR amplification of p27 CC and p16 DNAs. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a CC replication-deficient recombinant adenovirus that lacks functional CC large proteins, and comprises a transgene encoding a cyclin CC dependent kinase inhibitor (CDK1). The CDK1 is selected from an CC INK4 family protein such as human p16, a CIP/KIP family protein CC comprising (active fragments of these, or fusion proteins and CC CIP/KIP family protein (see AAY96046 and AAY96049). The method is used CC CIP/KIP family protein such muscle cell hyperproliferation, induced by injury caused by angioplasty, stent placement or vein crestenessis. Also claimed are recombinant lentiviruses encoding
                                                                                                                                                                                                                                                                                        Matches 121;
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Best Local
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05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant lentivirus for inhibiting proliferation muscle cells in e.g. restenosis, is replication deficient a transgene encoding a cyclin dependent kinase inhibitor {\bf r}
                                                                                                                                                                                                                                                                                                                                                                         Sequence
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N-PSDB; AAA50489.
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                                                                                    365 d
                                                                                                                                             305 vlhragarldvrdawgrlpvdlaeelghrdvarylraaaggtrgsnharidaaegpsdip
                                                                                                                    148 D 148
                                                                                                                                                                                                                     245 alpnapnsygrrpiqvmmmgsarvaellllhgaepncadpatltrpvhdaaregfldtlv 304
                                                                                                                                                                    88 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                     28 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
                                                                                                                                                                                                                                                                                                          Local Similarity
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99US-0163682.
99US-0457568.
                                                                                                                                                                                                                                                                                                        81.8%;
100.0%;
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                 2002, 17:28:32
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d comprises
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Run on: OM protein protein search, using sw model September 19, 2002, 17:27:07 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. ٠. ; Search time 16.1 Seconds
(without alignments)
883.306 Million cell updates/sec

Sequence: Title: Perfect score: US-09-016-869B-35 1 MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD 148

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

ize : 0

Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

PIR_71:*

pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 80 | 7 | υ. | 5 | 4 | ω | 2 | 1 | No. | Recult |
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| 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | œ | 80 | œ | œ | 19 | 34 | 48 | 72 | 121 | Score | |
| 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 5.4 | 5.4 | • | • | • | • | • | 48.6 | • | Match | & Operv |
| 229 | 227 | 223 | 223 | 223 | 216 | 205 | 195 | 173 | 171 | 171 | 166 | 166 | 164 | 160 | 154 | 142 | 141 | 138 | 138 | 1693 | 1691 | 390 | 334 | 167 | 41 | 130 | 138 | 156 | Length | |
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| H83425 | A75304 | D23724 | C23724 | B23724 | AH3203 | C89814 | T36141 | AI1885 | AF2864 | E97641 | B57378 | A57379 | A57378 | E34768 | A70792 | B72683 | AB1892 | AI1156 | AD1515 | MNWHE | A44212 | T43647 | G69303 | I58352 | I52720 | I78845 | 5547 | JE0141 | ID | |
| probable enoyl-CoA | ABC transporter, A | | alcohol dehydrogen | ≺ | ct | hypothetical prote | 0 | hypothetical prote | æ | hypothetical prote | cyclin-dependent k | 4 | cyclin-dependent k | _ | _ | _ | _ | 1 | hypothetical prote | | genome polyprotein | hypothetical prote | iron (III) ABC tra | NK4a - mo | gene p15INK4B prot | S | 4 inhibitor p1 | Ö | Description | |

| 75 | 74 | 73 | 72 | 1 | | 1 0 | 0 | n c | 7 C | ט ט | 2 | 64 | 63 | 62 | 61 | 60 | 59 | 58 | 57 | 56 | 55 | 54 | 53 | 52 | 51 | 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω 5 | 34 | 33 | 32 | 31 | 30 |
|--------|--------|----------------|--------|------------------|------------------|------------|---------------|---|----------------|--------|--------------------|-----|-----|--------------|--------|-----------|-----|--------|--------|--------|--------|--------------------|--------|-----------------|-------------|--------|--------|--------------------|--------|--------------------|-------------|------|-----|--------------------|-----|--------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------|-------------------|----------|
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| 4.7 | 4.7 | 4.7 | 4.7 | 4./ | . 4 . / | | | 4 · · · · · · · · · · · · · · · · · · · | 7 · | 4 7 | | 4.7 | 4.7 | 4.7 | 4.7 | | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | | | | | 4.7 | | | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 | 4.7 |
| 527 | 527 | 523 | 520 | 275 | 100 | 000 | 1 4 | л C > # | л н С | 479 | 466 | 464 | 462 | 413 | 405 | 389 | 365 | 364 | 363 | 353 | 348 | 348 | 346 | 345 | 334 | 333 | 331 | 318 | 314 | 283 | 278 | 273 | 254 | 254 | 254 | 254 | 254 | 254 | 254 | 254 | 254 | 254 | 254 | 251 | w | w |
| N | ш | N | ~ | ^ | ۸ (| ۸ د |) N |) h | J t | .) I | ٠ - | N | N | ν | N | 2 | N | N | N | N | N | Ν | N | 2 | N | 2 | 2 | ۳ | Ν | N | N | N | N | N | H | سا | μ | μ | ۲ | سو | Н | | Н | N | N | ν |
| T37055 | QRSEUB | 70 | | 1 4 | 12/ | | 1 0 | νo | 001 | | | Ħ | 7.5 | 7 | F86314 | E82618 | 8 | C70777 | E75457 | D75553 | T35450 | T18230 | C86413 | B84752 | A82751 | JC7713 | D86413 | F70536 | D70313 | E84258 | ~1 | 4 | | | | | 24 | B24268 | 90 | S15712 | 15 | A40553 | 퍾 | F82977 | 998 | A95886 |
| ğ | teir | robable purH p | TCaT I | xoporyphosphacas | xoporyphosphatas | ranol mbos | rgriffosectia | argininosuccinate | arginingsingth | obable | capsid protein ICP | | | ble transpos | F2H1! | hetical p | cys | | | | porter | alcohol dehydrogen | steine | obable cysteine | transporter | yrin-r | protei | 3',5'-cyclic-nucle | kinas | hypothetical prote | lybdenum tr | ical | | alcohol dehydrogen | ř | \mathbf{r} | alcohol dehydrogen | | alcohol dehydrogen | | alcohol dehydrogen | alcohol dehydrogen | alcohol dehydrogen | ŗ | purine nucleoside | le trans |
| | | | | | | | | | | | | | | | | _ | _ | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

C;Species: Homo sapiens (man)
c;Date: 02-Unn-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
C;Accession: JE0141; I59268; S39359; I59585; JC5679
R;Huang, C.G.; Deng, W.; Fu, J.L.
Chin. J. Biotechnol. 13, 105-107, 1997
A;Title: Molecular cloning and sequencing of P16 ink4 cDNA from hela cell.
A;Reference number: JE0141
A;Accession: JE0141
A;Accession: JE0141
A;Accession: JE0141
A;Accession: JE0141 cyclin dependent kinase inhibitor – human N; Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor

A; Molecule type: mRNA
A; Residues: 1-156 <HUA>
A; Residues: 1-156 <HUA>
A; Residues: 1-156 <HUA>
A; Experimental source: Hella cell
R; Okamoto, A; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett,
Proc. Natl. Acad. Sci. U.S.A. 91; 11045-11049, 1994
A; Title: Mutations and altered expression of p16INK4 in human cancer.
A; Reference number: I59268; MUID:95062202
A; Accession: I59268
A; Status: translation not shown; translated from GB/EMBL/DDBJ
A; Molecule type: DNA

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R; Hannon, G.J.; Beach, D.

Nature 371, 257-261, 1994

A; Title: p15(INK4B) is a potential effector of A; Reference number: S47593; MUID:94359613

A; Accession: S47593

A; Molecule type: mRNA
A; Residues: 1-19, 'TP', 22, 24-31, 'HSW', 35-138 <HJ
A; CYNSS-references: GB:L36844; NID:9556197; PII
A; Exportantal source: HaCaT cells
A; Kamb, M; Gruis, N.A.; Weaver-Feldhaus, J; 1
                                                                                                                                                                                                                                                                                                                                                                   A:Title: Growth suppression by p18, a p16(INK4/MTS1)-A;Reference number: A55479; MUID:95095079
A:Accession: B55479
A:Molecule type: mRNA
A:Residues: 1-138 <GUA>
A:Cross-references: GB:UJ7075; NID:9639715; PIDN:AAC50
A:Experimental source: HeLa cells
R:Hannon, G.J.; Beach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jul-2000
C;Accession: B55479; S47593; I81183; I52713
R;Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: this sequence is corrected in reference I59268 R;Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, Science 264, 436-440, 1994
A;Title: A cell cycle regulator potentially involved in genesis A;Reference number: I59585; MUID:94204645
A;Accession: I59585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C; Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-152 <OKA>
A;Cross references: GB:L27211; NID:g558656; PIDN:AAA92554.1; PID:g558657
A;Cross references: revised in GenBank entry HUMINK4X, release 113.0,
R;Serrano, M: Hannon, G.J.; Beach, D.
Nature 366, 704-707, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 9-34,'V',36-156 <SER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: translation not shown; translated from GB/EMBL/DDB
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Best Local Similarity 100.
Matches 121; Conservative
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100.0%; Pred. No. 2.2e-111;
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        J.; Liu,
                                                                               <HAN>
PIDN:AAA50282.1;
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    Harshman,
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    Tavtigian,
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    S.V.;
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gene p151NK4B protein - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision
C;Accession: I52720
                                                                               RESULT
I52720
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A;Gene: p151NK4b
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
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A;Cross-references: GDB:579577; OMIM:600431
A;Map position: 9p21-9p21
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C;Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-130 <RES>
A;Cross-references: GB:S79252; NID:g1087092; PID:g1087093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 11, 635-645, 1995
A;Tittle: Cloning and characterization of murine p16INK4a
A;Reference number: I58352; MUID:95380169
A;Accession: I78845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Mus sp. (mouse)
(;Pate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000 C;Accession: 17846
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C;Genetics:
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A; Accession: I52713
A; Status: preliminary; translated
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A;Reference number: I52713; MUID:95079408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.;
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A; Residues: 1-52 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 53-138 < KAM>
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A;Titlee A cell cycle regulator potentially involved in A;Reference number: I59585; MUID:94204645
A;Accession: I81183
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Matches 72
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72; Conser
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100.0%;
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Pred. No. 1.3e-39;
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10. 3.3e-63;
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26-Jul-1996 #text_change

26-May-2000

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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sysmith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing A;Reference number: A69250; MUID:98049343
A;Accession: G69303
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: I-334 <KLE>
A;Cross:references: GB:AE001075; GB:AE000782; NID:92689398; PIDN:AAB90806.1; PID:C;Superfamily: vitamin B12 transport protein btuC
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A;Nolecule type: mRNA
A;Residues: 1-167 <RES>
A;Residues: 1-16
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C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: 158352
R;Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Ricl Oncogene 11, 635-645, 1995
A;Title: Cloning and characterization of murine p16INK4a and p15INK4b genes A;Reference number: I58352; MUID:95380169
A;Accession: I58352
                                                                                                                                                                                                                                                                                                                                          R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Oyerbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Aug-1999
C;Accession: G69303
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C; Superfamily:
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C;Species:
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C;Superfamily: unassigned ankyrin
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A; Residues: 1-41 <RES>
A; Cross-references: GB
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A;Reference number: I52720; MUID:95228036
A;Accession: I52720
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Cancer Res. 55,
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No.
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Pred. No. 5.7e-:
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A:Cross-references: GB:M74506; NID:g33001; R;Fry, K.E.; Tam, A.W.; Smith, M.M.; Kim, Virus Genes 6, 173-185, 1992
A:Title: Hepatitis E virus (HEV): strain v A;Reference number: A48547; MUID:92271462
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Brovirology 191, 550-558, 1992
A;Title: Molecular cloning and sequencing of the Mexico isolate of A;Reference number: A44212; MUID:93079857
A;Accession: A44212
                                                                                                                                                                                      A;Note: sequence extracted from NCBI backbone (NCBIN:104576, NCBIP:104578) C;Superfamily: hepathitis E virus nonstructural protein c:Reywords: ATP; GTP binding; nonstructural protein; nucleotide binding; n F;973-980/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome polyprotein - hepatitis E virus (strain Mexico)
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: hepatitis E virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lee, M.; Yoo, H.S.; Chung, K.S. submitted to the EMBL Data Library, February A;Description: Clone 17 (bimD homologue).
                                                                                                                                                                  F;979/Binding site: ATP/GTP (Lys) #status predicted
                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA
A; Residues: 965-1691 <FRY>
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: genomic RNA
A; Residues: 1-1691 <HUA>
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A; Residues: 1-390 <LEE>
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A; Accession: T43647
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T43647
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A; Note: sequ
C; Superfamil:
C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A40778; A48547
R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G. Virology 185, 120-131; 1991
A;Title: Hepatits E virus (HEV): molecular cloning and sequencing of the full-length vi A;Reference number: A40778; MUID:92024067
A;Accession: A40778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O. D.; Jones, L.M.; Karst, U. Sience 294, 849-852, 2001

Chience 294, 849-852, 2001

Chors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AD1515
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C;Species: hepatitis E virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
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A;Molecule type: DNA
A;Residues: 1-138 <GLA>
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1515
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A; Residues: 1-1693 < TAM>
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ains: RNA-directed RNA polymerase
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olymerase (EC 2.7.7.48)
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                                                                                                                        hypothetical protein APE0883 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_ch C;Accession: B72683
                                            R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID:99310339
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RESUL, AI115

#text_change 09-Jun-2000

Та J.

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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11156
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number AB1807; MUID:21595285; PMID:11759840
A;Accession: AB1892
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A;Molecule type: DNA
A;Residues: 1-138 <GLA>
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A;Molecule type: DNA
A;Residues: 1-141 <KUR>
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C;Species: Anabaena sp.
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September 19, 2002, 17:28:57; Search time 11.94 Seconds (without alignments) 479.941 Million cell updates/sec
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Title:
Perfect score:
Sequence:

US-09-016-869B-35
148
1 MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD 148

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | Result No. |
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| | Score |
| 28 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | ery |
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| 75 | 74 | 73 | 72 | 71 | 70 | 69 | 68 | 67 | 66 | 65 | 64 | 63 | 62 | 61 | 60 | 59 | 58 | 57 | 56 | 55 | 54 | 53 | 52 | 51 | 50 | 49 | 48 | 47 | 46 | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | | 36 | 35 | |
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| 147 | 146 | 145 | 142 | 141 | 4 | 140 | w | 130 | 130 | 129 | 128 | 126 | 124 | 123 | 122 | 120 | 116 | 102 | 2397 | 2194 | æ | 889 | \circ | \circ | J | \vdash | 7 | 7 | w | N | N | d) | 9 | Q) | 4 | 9 | (J) | CJ1 | 253 | UT. | CT. |
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| NIRG_PSEST | HBB_CHEKU | 1 | UP12_ECOLI | HBA_CICCI | CALO_HUMAN | RINA_BPPHA | YCE3_HUMAN | TRJ5_ECOLI | RS9_STAAM | RS9_BACSU | | TYRT_STRAL | SGP2_CHRVI | | ₩ | R18E_AERPE | ı | CH15_DROGR | MOKB_SCHPO | GLSN_MEDSA | 1 | C122_HUMAN | UL17_HSVEB | UVRD_MYCTU | C2_ | | | ļ | 897 | SFUB_SERMA | PUR9_MYCTU | ٩ | VP19_HSV2G | MYCT | ADH2_CANAL | MYRA_MICGR | ADH_DROLE | ADH_DROSL | _DROP | ADH_DROPI | ADH_DRONI |
| 2524 | P80271 chelodonich | ð | 7 | P01983 ciconia cic | 258 homo | 82 bact | 3e2 | 7907 e | 52 | 1470 baci | 5 | 46 s | a | streptomyc | escherichi | aeropy | | Q, | schizosa | medic | homo | homo. | 8950 equine her | O53344 mycobacteri | mus muscul | 40 11 | | 39 escherichi | 0555 m | 21409 se | 71553 m bifur | 89461 herpes | 22486 herpes | 10503 mycobac | 038 candida al | 37000 | P10807 drosophila | 78 | 23277 | 361 | 00672 drosophi |
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ALIGNMENTS

| RA | RA | RX | RΡ | RN | RL | RT | RT | RA | RX | RP | RN | o X | 8 | 8 | SO | GN | DE | DE | DT | DT | DT | AC | ID | CDN2 | RESULT |
|--|---|-----------------------------------|------------------------------|-----|---------------------------|--------------------------------|--|------------------------------------|-----------------------------------|--------------------|-----|------------------|--|---|-----------------------|------------------|---------------------------------------|--|---|---|--------------------------------|-----------------|-----------------------------------|------------|--------|
| Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E., | Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K., | MEDLINE=94204645; PubMed=8153634; | SEQUENCE OF 51-152 FROM N.A. | [2] | Nature 366:704-707(1993). | inhibition of cyclin D/CDK4."; | "A new regulatory motif in cell-cycle control causing specific | Serrano M., Hannon G.J., Beach D.; | MEDLINE=94081956; PubMed=8259215; | SEQUENCE FROM N.A. | [1] | NCBI_TaxID=9606; | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Homo sapiens (Human). | CDKN2A OR CDKN2. | (Multiple tumor suppressor 1) (MTS1). | Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A) | 01-MAR-2002 (Rel. 41, Last annotation update) | 15-JUL-1998 (Rel. 36, Last sequence update) | 01-NOV-1995 (Rel. 32, Created) | P42771; Q15191; | CDN2_HUMAN STANDARD; PRT; 156 AA. | CDN2_HUMAN | LT 1 |

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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Hayward N.K., Fountain J.W.
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EMBL; U12818; AAB6064
EMBL; U12819; AAB60648
EMBL; S69804; AAD14048
EMBL; S49804; CAA6387
PDB; 1BT7; 16-FEB-99.
PDB; 1DC2; 23-DEC-99.
                                                                                                                                                                                                                           CDN5_HUMAN
P42772;
01-NOV-1995
                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor B (P14-INK4B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; Li-Fraumeni syndrome; REPEAT 1 40 ANK 1. REPEAT 44 72 ANK 2. REPEAT 77 106 ANK 3. REPEAT 110 139 ANK 4. VARIANT 14 14 D -> E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an
                             "Growth suppression by p18, a p16INK4/MTS1-CDK6 inhibitor, correlates with wild-type pRGenes Dev. 8:2939-2952(1994).
                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                    (Multiple tumor
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PROSITE; PS50088; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
 MEDLINE=94359613;
          SEQUENCE FROM N.A.
                                                                 Matera G.A., Xiong Y.;
                                                                                      SEQUENCE FROM N.A.
MEDLINE=95095079; PubMed=8001816;
                                                                                                                        NCBI_TaxID=9606
                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                HUMAN
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                                                                                                                                   Eutheria;
                                                                                                                                                                               tumor suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
ilarity 100.0%;
Conservative
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AAB60645.1; JOINED.
AAB60645.1; JOINED.
AAD14048.1; CAA63870.1; -.
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                                                                                                                                                                                                                                                    STANDARD;
PubMed=8078588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANK_REPEAT; FALSE_NEG
                                                                            C.W., Li
                                                                                                                                    Primates;
                                                                                                                                             Chordata;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILIAL MELANOMA).
                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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A -> P (IN A LUNG
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                                          pRb function
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                                                                            W<sub>L</sub>
                                              p14INK4B/MTS2-related
unction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 156;
                                                                            X., O'Keefe
                                                                                                                                                                                            (P15-INK4B)
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHI POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
-!- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
-!- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primary and metastatic lung cancer."; Cancer Res. 55:1448-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS LUNG ADENOCARCINOMA GLU-47 AND MEDLINE-95188190; PubMed-7882351; Okamoto A., Hussain S.P., Hagiwara K., Sometiti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 types.";
Science 264:436-440(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamb A., Gruis N.A., Weav
Tavtigian S.V., Stockert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arrest."
                                                                                                                                                                                                                          EMBL; U17075; AAC50075.1; -. EMBL; L36844; AAA50282.1; -. EMBL; S69805; AAD14049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demetrick D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hannon G.J., Beach D.;
"p15INK4B is a potential effector of TGF-beta-induced cell cycle
                                                                                                                               PROSITE; PS50297;
Cell cycle; Anti-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Demetrick D.J., Serrano M., Hannon G.J., Shiseki M.,
Xiong Y., Beach D.H., Yokota J., Harris C.C.,
"Mutations in the pl6INK4/MTS1/CDKN2, pl5INK4B/MTS2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A cell cycle regulator potentially involved in genesis of many tumor
                                                                   VARIANT
                                                                                            VARIANT
                                                                                                                                                          PROSITE; PS50088; ANK_REPEAT;
                                                                                                                                                                         Pfam;
                                                                                                                                                                                                   MIM; 600431;
                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 2 ANK REPEATS
                                                                                                         REPEAT
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                                                                                                                                                                                       InterPro; IPR002110;
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                                                                                                                                                                       PF00023;
                                                                                                                                                                                                               P42771; 1BI7.
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20
23
32
138
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73
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Serrano M., Hannon G.J
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47
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kert E., Day R.S.
    MW;
                                                                                                                                 Repeat;
  MISSING (IN REF. 2).
QLL -> HSW (IN REF. 2).
; 0D6FFBDFA6FEAD21 CRC64;
                                       /FTId=VAR_001489.
SA -> TP (IN REF. 2).
                                                                  /FTId=VAR_001488
A -> V (IN LUNG
                                                                                                        ANK 2.
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                                                                                                                   (INCOMPLETE).
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I, Johnson
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                                                                  ADENOCARCINOMA)
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son B.E.,
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Best Local
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                     AWGRLPVDLAEE 112
                                                                   IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 100
AWGRLPVDLAEE 122
                                            IQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 110
                                                                                                   Similarity
                                                                                         Conservative
                                                                                                   48.6%;
100.0%;
                                                                                         0;
                                                                                                   Score 72;
Pred. No.
                                                                                           Mismatches
                                                                                                  DB 1; Le 8.1e-63;
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Best Local S
Matches 48
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
[1]
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                       Cell
                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK. Pfam; PF00023; ank; 3. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                           EMBL; U66085; AAB39833.1
EMBL; U66084; AAB39833.1
HSSP; P42771; 1BI7.
MGD; MGI:104737; Cdkn2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alterations in murine primary T-cell lymphomas.";
Oncogene 14:1361-1370(1997).
-i- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97322242; PubMed-9178896; Malumbres M., de Castro I., Santos J., Melendez B., Mangues R. Serrano M., Pellicer A., Fernandez-Piqueras J.; "Inactivation of the cyclin-dependent kinase inhibitor p151NK41 deletion and de novo methylation with independence of p161NK4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE—95380169; PubMed=7651726;

MEDLINE—95380169; PubMed=7651726;

Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Tro
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;

"Cloning and characterization of murine pl6INK4a and p15IN
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDN5_MOUSE STANDARD; PRT; 130 AA. P55271; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
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STRAIN-C57BL/6J X DBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
            ,51 VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV 98
                                                                                                                                                                                       REPEAT
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                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
53\VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY) TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY. INDUCTION: BY TGF-BETA.
SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE SIMILARITY).
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                                                                                                                                                                                                                      cycle;
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48; Conserv
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le; Anti-oncogene; Repeat; ANK repeat.

5 34 ANK 1.

38 66 ANK 2.

71 100 ANK 3.
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130 AA;
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AAB39833.1;
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Pred. No.
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                                                           Mismatches
                                                                          DB 1; L:
. 1.7e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95228036; PubMed=7712460;
Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;
"Association of rat p151NK4B/p161NK4 deletions with monosomy
kidney epithelial cell lines but not primary renal tumors.";
Cancer Res. 55:1607-1612(1995).
                                                                                                                                                                                                                                                                                                                                     EMBL; S79760; AAB35360.1; EMBL; S77734; -; NOT_ANNO HSSP; Q60773; 1AP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular genetic basis of renal carcinogenesis model of tuberous sclerosis (Tsc2).";
Mol. Carcinog. 14:23-27(1995).
  SEQUENCE
                                                                                                                                                  CHAIN
                                                                                                                                                                                                                           PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                      InterPro; IPR002110; ANK. Pfam; PF00023; ank; 3. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-96001392; PubMed-7546221;
Hino O., Kobayashi E., Hirayama Y.,
Tsuchiya H., Kikuchi Y., Mitani H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDKN2B OR INK4.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 46-86 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF P14 WITH CDK4.
ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY
INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INHIBITORS.
SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INTERACTS STRONGLY WITH CDK4
POTENTIAL EFFECTOR OF TGF-BETA INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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                                                                                                                                                                                                            cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
    30
                                                                                                                                                                                                            Anti-oncogene;
                                             46
38
71
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                                                                                                                                                                                                                                                                                                                                                          NOT_ANNOTATED_CDS.
46
34
66
100
130
13748
                                                                                                                                                130
  WW;
                                                                                                                                                               Repeat; ANK repeat; Alternative initiation CYCLIN-DEPENDENT KINASE 4 INHIBITOR B, LONG ISOFORM.
                                      CYCLIN-DEPENDENT KINASE 4
SHORT ISOFORM.
FOR SHORT ISOFORM.
ANK 1.
ANK 2.
ANK 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
  AC45B21FA69FAD92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kobayashi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF CYCLIN-DEPENDENT KINASE
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Query Match
Best Local Similarity

24.3%; 100.0%;

Score Pred.

36; No.

DB 1; L₁ 7.8e-28;

Length 130;

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Matches 19
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HSSP; Q60773; 1AP7
MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 3.
SMART; SM00248; ANK; 1.
                                                                                              REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _MOUSE
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                   PROSITE; PS50088; ANK_REPEAT; FALSE_NEG.
PROSITE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Anti-oncogene; Repeat; ANK repeat;
CHAIN 1 167 CYCLIN-DEPENDENT K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2091 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor A (CDK4I)
CDKN2A OR P16INK4A.
                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                       -i- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-i- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=9538019; PubMed=7651726;
Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano
"Cloning and characterization of murine pl61NK4a and pl
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P51480;
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    71
                        72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEI BAILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6. SUBJUNT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                           CONTAINED CDK6
                       RPVHDAAREGFLDTLVVLH
                                                                                                                                                                                                                                                                                                                                                                                 INHIBITORS.
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                                           . Similarity
19; Conser
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                                                                                                                                                                                                                                                                                requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                 43
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                                                                                                                                                                                                                                                                                                                                                                      CONTAINS 2 ANK REPEATS
                                                                                             130
17870
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63
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                                                                                                                            SHORT ISOFORM.
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                                                                                                                                                           LONG ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                            88C4588A105ECB8F CRC64;
                                           Mismatches
                                                                                                                             SHORT ISOFORM
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                                                                                                                                                                RINASE 4 INHIBITOR A,
                                          0;
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                                                              Length 167;
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RESULT 6
CDN2_MONDO
ID CDN2_MONDO
AC 077617;
DT 15-JUL-1999
DT 15-JUL-1999
                                                                                          RESULT 7
V222_FOWPV
                                                                                                                                                                                                                                                             Query Match
Best Local
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V222_FOWPV
Q9J513;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherburn T.E., Gale J.M., Ley R.D.;
Submilted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
Submilted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIL
ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLLFERATION OF NORMAL CELLS (BY SIMILARITY)
-!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY)
-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF064808; AAC23669.1;
EMBL; AF064808; AAC23670.1;
HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Cyclin-dependent kinase 4 inhibitor A (CDK41) (P16-INK4) (P16-INK4A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Cl
Mammalia; Metatheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00023; ank;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=13616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monodelphis
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                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor suppressor CDKN2A).
                                                                                                                                                                                                     73 PVHDAAREGFLDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cycle; Anti-oncogene;
N 1 171
                                                                                                                                                                  PVHDAAREGFLDTL 128
                                                                                                                                                                                                                                          l Similarity
14; Conserv
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171
 (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domestica (Short-tailed grey opossum).
Metazoa; Chordata; Craniata; Vertebrata;
etatheria; Didelphimorphia; Didelphidae;
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               35
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                                                                         STANDARD;
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 Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; ANK repeat; Alternative initiation. CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                             Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   CYCLIN-DEPENDENT KINASE 4 INHIBITOR SHORT ISOFORM.
FOR SHORT ISOFORM.
ANK 1.
ANK 2.
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                                                                         PRT;
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                                                                                                                                                                                                                                            Mismatches
                   update)
                                                                         747
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2.5e-06;
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DT 01-OCT
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OS Hepati
OC Viruse
OX NCBL_T
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Q1-OCT-1993 (Rel. 27, Created)
Q1-OCT-1993 (Rel. 27, Last sequence update)
Q1-OCT-2001 (Rel. 40, Last annotation update)
Non-structural polyprotein [Contains: RNA-directed RNA polymerase (BC 2.7.7.48); Helicase].
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                                                             Hepatitis E virus (strain Mexico) (HEV). Viruses; ssRNA positive-strand viruses, INCBI_TaxID=31768;
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           Huang C.C., Nguyen D., Fernandez J., Bradley D.W., Tam A.W., Reyes G.R.;
                                SEQUENCE FROM N.A. Mr.DLINE=93079857; PubMed=1448913;
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MEDLINE=20193820; PubMed=10729156;
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PROSITE; PS50297; ANK_REP_REGION;
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Best Local Similarity 100.
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Pfam; PF01978; RNA_dep_RNApo12; 1.
Pfam; PF01443; Viral_helicase1; 1.
Pfam; PF01660; Vmethyltransf; 1.
SMART; SM00506; Alpp; 1.
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                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., H
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular
                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Non-structural polyprotein [Contains: RNA-directed RNA
(EC 2.7.7.48); Helicase].
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region encoding consensus motifs for
and an ATP/GTP binding stite.";
Virus Genes 6:173-185(1992).
-i- MISCELLANEOUS: HEPATITIS E VIRUS
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Fry K.E., Tam A.W., Smith M.M., Kim J.P., Luk K.C., Young I
Piatak M., Feldman R.A., Yun K.Y., Purdy M.A., McCaustland
Bradley D.W., Reyes G.R.;
                                           full-length viral genome.";
Virology 185:120-131(1991).
-!- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT
                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, NCBI_TaxID=31767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
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                     ENTERICALLY TRANSMITTED NON-A,
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Copyright (c) 1993 - 2000 Compugen Ltd
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Q9upb7 homo sapien
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ALIGNMENTS

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AC Q9NP05; PRELIMINARY; PRT; 106 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-DCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE CDK41 PROTEIN (FRAGMENT).

GN CDK41.
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                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ery Match
                                                                                                                                                                                                                                                                                                                                                          Q9GMF2 PRELIMINARY; PRT; 81 AA.
Q9GMF2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seguence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
Q9XS52
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Venkatraj V.S., Mayor J., Modiano J.F.; venkatraj V.S., Mayor J., Modiano J.F.; "Role of p16/Ink4-a in familial canine cancers."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF234176; AAG01087.1; -. HSSP; P42771; 1B17.
                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94203288; PubMed=8152487;
Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson "Deletions of the cyclin-dependent kinase-4 inhibitor gene in human cancers.";
Nature 368:753-756(1994).
                                                                                                                                                                                                          InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S69824; AAD14050.1; -.
EMBL; S69822; AAD14050.1; JOINED
HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANK repeat; Repeat.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                        43 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                       w
                                                                                                                                                                                                  repeat; Kinase; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ν
                                                                                                     Similarity
54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AA; 11314 MW;
                                                                                                                                                                81
                                                                                                    36.5%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
PRELIMINARY;
                                                                                                                                                                          81
                                                                                                                                                                A,
                                                                                                                                                                8868 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                              Carnivora;
                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.6%;
                                                                                                     0;
                                                                                                   Score 54; DB Pred. No. 2.1 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106;
Pred. No.
                                                                                                                                                                0E39D8D805BEACOF CRC64;
                                                                                                                                                                                                                                                                                                                             Craniata; Ver; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2D59442F956B6A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                 DB o,
3. 2.1e-43;
0;
86
                                                                                                                                                                                                                                                                                                                              Vertebrata;
ia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8e-92;
ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                           Length 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 106;
                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
                                                                                                                                                                                                                                                                                                                              Euteleostomi; Canis.
                                                        80
                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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n multiple
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                       0;
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QΥ

62

PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 112

Matches

Conservative

0;

Mismatches

Indels

0

Gaps

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RESULT
Q9XS51
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                Query Match
Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.; "Cloning and chromosomal mapping of the feline genes pl6(MTS1, and pl5(MTS2/CDKN2B)."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB010808; BAA33541.1; -. HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9XS52:
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P15/MTS2/CDKN2B (FRAGMENT).
                                                                                                                  InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 3.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                     and p15(MTS2/CDKN2B)."; Submitted (JAN-1998) to the
                                                                                                                                                                                                                           TISSUE=PERIPHERAL BLOOD;
Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M.,
Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANK repeat; Repeat.
NON_TER 1
SEQUENCE 86 AA;
                                                                   SEQUENCE
                                                                              ANK repeat; Repeat.
NON_TER 1
NON_TER 102
                                                                                                                                                           EMBL; AB010807; BAA33540.1; HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              P16/CDKN2A/MTS1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                Q9XS51;
                                                                                                                                                                                                                                                                                                                                                                                                             Q9XS51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9685;
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                                                                                                                                                                                                             "Cloning and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 34.5%;
Similarity 100.0%;
51; Conservative
                                                                   102
102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANK_REP_REGION;
                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9340 MW;
                                                                   10824 MW;
                34.5%;
100.0%;
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Last sequence up
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              Score 51;
Pred. No.
                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
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Pred. No. 1.5e-40;
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                                                                   26399FF21359F35D CRC64;
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                                                                                                                                                                                                                of the feline
DB 6; LC.
0. 1.8e-40;
0;
                                                                                                                                                                                                                                                                                                                                                                                                             102
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                                                                                                                                                                                                                                                                                                                                                          update)
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                           Length 102
                                                                                                                                                                                                             genes p16(MTS1/CDKN2A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                        Euteleostomi;
Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
Felis.
                                                                                                                                                                                                                                         Endo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE

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RESULD OF RESULD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pellicer A., Fernandez-Piqueras J.;

Comparative analysis of the pl6(INK4a) and pl5(
In mouse inbred strains ";

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ dat
R EMBL; U79639; AAD00234.1; -.
R EMBL; U79638; AAD00232.1; -.
R EMBL; U79638; AAD00233.1; -.
HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 48
Oncos
EMBL; AF01540v,...
HSSP; P42771; 1BI7,
InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_RSP_REGION; 1
PROSITE; PS50297; ANK_RSP_REGION; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               054846 PRELIMINARY:
054846; TIEMBLEEL 0
01-JUN-1998 (TIEMBLEEL 0
01-JUN-1998 (TIEMBLEEL 0
01-DEC-2001 (TIEMBLEEL 1
CYCLIN-DEPENDENT KINASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9QUPO
Q9QUPO;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANK repeat;
NON_TER
NON_TER
SEQUENCE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
CYCLIN-DEPENDENT KINASE
                                                                                                                                          Oncogene 18:385-396(1999).
EMBL; AF015460; AAB94534.1;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
MEDLINE=99124385; PubMed=9927195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002110; ANK,
PROSITE; PS50297; ANK_REP_REGION;
ANK_repeat; Cyclin; Kinase; Repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
                                                                                                                                                                                                                Malumbres M., de Castro I.P., Santos J., Piqueras J.F., "Hypermethylation of the cell cycle inhibitor p15INK4b region interferes with its transcriptional regulation i
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDKN2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                       Lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13, Created)
13, Last sequence update)
19, Last annotation update)
19HIBITOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06, Created)
06, Last sequence update)
19, Last sequence update)
19, Last annotation update)
INHIBITOR P15INK4B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB; Pred. No. 1.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
1.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                     Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                       Pellicer A.;
3'-untranslated
                                                                                                                                                                                                                primary
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                                                                                                                                                                                                                                                                                                                                                                                                          Mus.
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PROBLET CONTROL OF CON
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AC Q0
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Best Local S
Matches 48
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                               Q9TSY1;
Q9TSY1;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9Z1C1
Q9Z1C1;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2QQ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....yota; Metazoa; Chordata; Cran
Mammalia; Eutheria; Rodentia; Sciu
NCBI_TaxID-10096;
sequences.";
Submitted (JUN-1999) to the
EMBL; AJ242787; CAB65454.1;
                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANK repeat; Kinase; Repeat.

NON_TER 1 1

NON_TER 86 86

SEQUENCE 86 AA; 9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; PROSITE; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pellicer A., Fernandez Piqueras J.;
"Comparative analysis of the pl6(INK4a)
in mouse inbred strain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                          STRAIN=LARGE WHITE;
Le Chalony C., Hayes
"Identification and r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-SPRET/EI;
                                                                                                                                                                                                                                             CDKN2A
                                                                                                                                                                                                                                                                CYCLIN-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U79637; AADO
HSSP; P42771; 1BI7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P15(INK4B).
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 32.4%;
Similarity 100.0%;
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OCT-1996)
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9269 MW;
                                                            mapping
                                                                                                                                                                                Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.4%;
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    Created)
    Last sequence update)
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10, Last sequence update)
19, Last annotation update)
INHIBITOR PROTEIN (FRAGMENT).
                                                            Frelating of s
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                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB
Pred. No. 1.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB Pred. No. 1.10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0499DB26144FB6DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509D9B3613251B18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p16(INK4a) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                            t G., G
                                                            Geffrotin C
e CDKN2A and
                                                                                                                                                                                                                                                                                                                                                               103
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1.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malumbres M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                 CDKN2B exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86
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                                                                                                                                                                                  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
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RESULT
Q9UBB7
ID Q9
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Best Local
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NON_TER
NON_TER
SEQUENCE 1
                                                                                                                                                                                                                                        01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91YF9 PRELIMINARY; PRT; 130 AA. Q91YF9; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) p.151NK4B CYCLIN-DEPENDENT KINASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Homozygous Deletion of p15INK4b/p16INKa Gene Locus in Syrian Golden Hamster Tumor Cell Lines."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ302037; CAC67498.1; - Kinase; Cyclin. Kinase; Cyclin. 30 AA; 13842 MW; 4C04DD3F8C6FF013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE From
SEQUENCE FROM
TISSUE-PANCREAS;
TISSUE-PANCREAS;
Melvin S., Pour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muscarella P., Ulric
Wittel U.A., Melvin
Weghorst C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                   Q9UPB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus (Golden hamster).
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SEQUENCE FROM N.A.
Murthy S.K., Demetrick D.J.;
"Genomic sequence of CDKN2A
                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                            CDKN2A.
                                                                                                                                                                                                                  CYCLIN-DEPENDENT
                                                                                                                                                                                                                                                                                                             Q9UPB7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLTRPVHDAAREGFLDTLVVLHRAGARLDVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLTRPVHDAAREGFLDTLVVLHRAGARLDVRD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE
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Pr00023; ank; 2.
TE; PS50297; ANK_REP_REGION;
epeat; Kinase; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P42771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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103 AA;
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) (TrEMBLrel.
1 (TrEMBLrel
ENDENT KINASE
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                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Rodentia;
                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11023 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.6%;
                                                                                                                                                                                                             13, Created)
13, Last sequence update)
19, Last annotation updat
INHIBITOR 2A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B., Casto B.C., Pour P.M., Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB Pred. No. 1.1 0; Mismatches
  (p16INK4A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score :
                                                                                                                     Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5D23ABCC1088DE0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Lu., 1.1e-36; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
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       ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moniaux N., Knobloch
H., Gold B., Batra S.
                                                                                                                       Vertebrata; Euteleostomi;
i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
2.1
                                                                                                                                                                                                                                                                                                                                     AA
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                                                                                                                                                                                                                                        update)
       ORF.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 130;
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Cricetinae;
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SEQUENCE
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095440;
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         MEDLINE=99373016;
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SQ SQ
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01-MAY-2000 (Trem)
01-DEC-2001 (Trem)
CYCLIN-DEPENDENT
                                                 Homo sapiens (Human).
Homo sapiens (Human).
'harvota; Metazoa; Chordata;
'harvota; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20290998; PubMed=10828598; Le Chalony C., Hayes H., Frelat G., Geffrotin C.; Le Chalony C., Hayes H., Frelat G., Geffrotin C.; "Identification and mapping of swine cyclin-dependent kinase inhibitor CDKN2A and CDKN2B exon2 sequences."; Cytogenet. Cell Genet. 88:240-243(2000). Cytogenet. Cell Genet. 88:240-243(2000). EMBL; AJ242788; CA865455.1; -. HSSP; P42771; 1817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ANK repeat; Kinase; Repeat.
NON_TER 1 1
SEQUENCE 86 AA; 9286 MW;
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pfam; pF00023; ank; 2.
pROSITE; pS50297; ANK_REP_REGION;
                                                                                                                             01-MAY-1999 (TYEMBLIEL. 10, Created)
01-MAY-1999 (TYEMBLIEL. 10, Last sequence update)
01-DEC-2001 (TYEMBLIEL. 19, Last annotation updat
CYCLIN-DEPENDENT KINASE INHIBITOR P12.
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TISSUE-PANCREAS
               SEQUENCE FROM N.A.
                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                62 PNCADPATLTRPVHDAAREGFLDTLV
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26; Conser
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nilarity 100.0%;
Conservative 0
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
NDENT KINASE INHIBITOR P15 (FRAGMENT).
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6 AA;
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3672
                                                                                                                                                                                                                                                                                                                                                                                                                                               9286 MW;
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Pred. No.
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Pred. No. 6.8e-17;
0; Mismatches 0;
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                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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PubMed=10445844

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Q9Z1C2
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01-MAY-2000
01-DEC-2001
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"Issue-specific alternative splicing in cycle regulatory locus."
Oncogene 18:3810-3820(1999).
EMBL; AF115544; AAD11437.1; -.
InterPro; IPRO02110; ANK_EMP_REGION; 1.
PROSITE; PS50297; ANK_EMP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29QWH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                               Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis o", the p16(INK4a) and p15(INK4b) I
in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MUS MUS POSCHIAVINUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANK repeat; Kinase; SEQUENCE 116 AA;
                                                     01-MAY-1999 (TIEMBLIEL. 10, Created)
01-MAY-1999 (TIEMBLIEL. 10, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                            Santos J., Melendez B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYCLIN-DEPENDENT KINASE
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         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                               Mus spretus (Western wild
                                            P16(INK4A).
                                                                                                   Q9Z1C2;
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                                                                                                                                                                                                                                                                                                                  PROSITE; PS50297; ANK_REP_REGION;
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NCBI_TaxID=10096;
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                                                                                                                                                                                                                                                                                                          repeat; Kinase; Repeat
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12212 MW;
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100.0%;
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Piqueras J.;
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13, Last sequence update)
19, Last annotation update)
INHIBITOR PROTEIN (FRAGMENT).
                                                                                                                                                                      48
                                                                                                                                                                                                                                                                         MW;
                               mouse).
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Pred. No.
         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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RESULT
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Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Santos J., Melendez B., Perez de Castro I., Malumbres Nellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) in mouse inbred strains.";
Submitted (OCT-1956) to the EMBL/GenBank/DDBJ databases EMBL; U79634; AAD00236.1; -...
HSSP; P42771; 1B17.
                                                                                                                                                                        PROSITE; PS5
ANK repeat;
SEQUENCE 1
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                                                                                                                                                                                                                                                                                 Swafford D.S., Middleton S.K., Palmisano W.A., Nikula K.J., Tesfaigzi J., Baylin S.B., Herman J.G., Belinsky S.A.; "Frequent aberrant methylation of pl6INK4a in primary rat lung
                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
STRAIN=F344/N; TI
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PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                        InterPro; IPR002110; A Pfam; PF00023; ank; 4. SMART; SM00248; ANK; 1
                                                                                                                                                                                                                                         EMBL; L81167; AAD48924.1; HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                  STRAIN=F344/N; TISSUE=LUNG; MEDLINE=97184461; PubMed=9032263;
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                                                                           RPVHDAAREGFLDTLVVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 12.8%; Similarity 100.0%; 19; Conservative
                                                                                                                                                                                               PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                              IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
113 AA;
                                                                                                                                                                          ; Repeat.
159 AA;
                                                                                                                                                                                                                                                               Biol.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                              17:1366-1374(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
12073 MW;
                                                                                                                                                                          17366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANK.
                                                                                                                              12.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score 19; DB; Pred. No. 3.6
0; Mismatches
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                               Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                          3C4CA920A1FEAEB6 CRC64;
                                                                                                                     Mismatches
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                                                                                                                                No.
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3.6e-10;
                                                                                                                               DB 11;
4.9e-10;
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                                                                                                                                          Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                          Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serrano
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089088; 01-NOV-1998

(TrEMBLrel. 08,

Created

PRELIMINARY;

168

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RESULT
P97510
ID P97510
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                                                                                                                                   P97510; P97937;
01-MAY-1997 (TYEMBLrel. 03, Created)
01-MAY-1999 (TYEMBLrel. 10, Last sequence update)
01-DEC-2001 (TYEMBLrel. 19, Last annotation update)
01-DEC-2001 (TYEMBLREL. 19, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
CDKN2A OR EIALPHA OR P16INK4A.
                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piam; PF00023; ank; 4.

SMART; SM00248; ANK; 1.

PROSTITE; PS50297; ANK_REP_REGION; 1.

ANK repeat; Cyclin; Kinase; Repeat.

ANK repeat; Cyclin; Kinase; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the pl6(INK4a) and pl5(INK4b) DNA
in mouse inbred strains."
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    P97510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a p19ARF, is a candidate for the plasmacytoma susceptibility locus Pctrl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang S.,
"Cdkn2a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A TUMOR SUPPRESSOR
PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
CDKN2A OR E1ALPHA OR P16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
Santos J., Melendez B., Perez de Castro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-42
STRAIN-MA/M4J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-42 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence variation and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97179476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98151529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPVHDAAREGFLDTLVVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPVHDAAREGFLDTLVVLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3151529; PubMed=9482902; Ramsay E.S., Mock B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8:65-66(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9021155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-SPLEEN;
                                                                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinase; Repeat.
17915 MW; 356A973BEAC4D167 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB Pred. No. 5.1 0; Mismatches
                                                                        Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95:2429-2434(1998).
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                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                     Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
5.1e-10;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                              ΑĀ
                                                                             Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             murine Cdkn2a
                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Mus
                                                                          Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serrano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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HSSP; P42771; 1B17.
MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; ANK.
                                                                                                                                                             EMBL;
                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                    "Cloning and structure analysis of murine pl6INK4a.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databas
EMBL; AF044336; AAC08963.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Santos J., Melendez B., Perez de Castro I., Pellicer A., Fernandez-Piqueras J.; "Comparative analysis of the p16(INK4a) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DBA/2, AND C57BL/6;
MEDLINE-95380169; PubMed=7651726;
Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
"Cloning and characterization of murine pl6INK4a and pl5INK4b genes.";
oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                        "Cloning and structure
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129/SVJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98151529; PubMed=9482902; Zhang S., Ramsay E.S., Mock B.A.; "Cdkn2a, the cyclin-dependent kinase inhibitor encoding pl6INK4a and pl9ARF, is a candidate for the plasmacytoma susceptibility locus, Pctrl.";
                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 180:213-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soloff E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=DBA/2, AND C57BL/6; Gressani K.M., Rollins L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-42 FROM N.A. STRAIN-DBA/2, AND C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6J X DBA;
Malumbres M., de Castro I., Santos J., Melendez B., Manserano M., Pellicer A., Fernandez-Piqueras J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                    PROSITE;
                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in mouse inbred strains.";
Submitted (OCT-1996) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CAST/EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The 5'-flanking region of the E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97128829; PubMed=8973369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ICR SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         suppressor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MTS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VARIOUS STI
MEDLINE=97179476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DBA/2N; TI:
MEDLINE=98151529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence variation and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derzog C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                         AF004588; AAB61416.1; -..; U47018; AAC52987.1; -..; U79628; AAD00226.1; -..; U79625; AAD00225.1; -..; U79627; AAD00225.1; -..;
                                   PF00023; ank; 4. SM00248; ANK; 1.
                                                                                                                                                                                                                                                         U49280; AAC00052.1; -.
U66087; AAB39600.1; -.
U66086; AAB39600.1; JOINED
                                                                                                                                          AF332190;
                  PS50297;
Cyclin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herzog C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8:65-66(1997).
                                                                                                                   0; AAK83159.1;
1BI7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FROM N.A.
C57BL/6J, ARF/J, AND MOLF/EI;
Parez de Castro I., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
              ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9021155;
Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       You M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller M.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p15(INK4b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malumbres M.,
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Q9QWH8;
01-MAY-2000
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Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TREMBLREL 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases EMBL; U79630; AAD00227.1; -. HSSP; P42771; 1BI7.
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STRAIN-(57BL/6J, RF/J, AND CAST/EI;
STRAIN-(57BL/6J, RF/J, AND CAST/EI;
Santos J., Melendez B., Perez de Castro
Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Mus musculus (Mouse)
                                                                                                                                                                             Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
  Santos J., Melendez B., Perez de Castro Pellicer A., Fernandez-Piqueras J.; "Comparative analysis of the p16(INK4a) in mouse inbred strains.";
                                                                                                       SEQUENCE FROM N.A. STRAIN-BALB/CJ;
                                                                                                                                                                                                                                                                                       P16(INK4A).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QWH7
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Pred. No.
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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5.1e-10;
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! 01-MAY-2000 (TrEMBLrel. 13,
T 01-MAY-2001 (TrEMBLrel. 13
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in mouse inbred strains.";
in mouse inbred (CCT-1996) to the EMBL/GenBank/DDBJ
cohmitted (CCT-1996); -.
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pr0SITE; pS50297; ANK_REP_REGION;
                                                          097886; PRELIMINARY; PRT; 58 AA.
097886; 01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
CDKN2A.
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SEQUENCE 113 AA; 12147 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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PROSITE; PS50297; ANK_REP_REGION;
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             Equus caballus (Horse).
Eukaryota; Metazoa; Chordata;
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113 AA;
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; 12147 MW;
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Rodentia;
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13, Last sequence update)
19, Last annotation update)
INHIBITOR PROTEIN (FRAGMENT).
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Pred. No.
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Pred. No.
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               Craniata;
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3.2e-09;
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3.2e-09;
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                  Vertebrata;
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                  Euteleostom1;
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                                   RESULT 23
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Best Local Similarity 100.0%;
Matches 15; Conservative
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"Comparative analysis of the pl6(INK4a) and pl
in mouse inbred strains.";
Submitted (CCT-1996) to the EMBL/GenBank/DDBJ
EMBL; U79633; AADD0230.1; -.
HSSP; P42771; 1BIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9QWH5 PRELIMINARY; PRT; 113 AA.
Q9QWH5;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
 00an60
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Pfam; PF00023; ank; 1.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1998) to the EMBL; AF076782; AAC97110.1; HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Santos J., Melendez B.,
Pellicer A., Fernandez-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.; "An equine sequence homologous to cyclin-dependent kinase (CDKNZA).";
                                                                                                                                                                                                                                                                                          ANK repeat; Kinase; Repeat.
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MUS MUS MUSCULUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                               NON TER
                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR002110; ANK.
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Local Similarity 100.0%
Les 15; Conservative
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                                                                                                               RPVHDAAREGFLDTL 86
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                                                                                           RPVHDAAREGFLDTL
                                                                                                                                                                                                                                                         113
113 AA;
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 PRELIMINARY;
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                                                                                                                                                               Score 15; DB 11;
Pred. No. 2.2e-06;
0; Mismatches 0;
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Pred. No. 1.2e-(
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 PRT;
                                                                                                                                                                                                                                                           5D4DE8325D06638B CRC64;
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 21
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es 0;
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Q9EQ33
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Q99PH0
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Best Local S
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Matches 12
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2000 (TrEMBLrel. 14, Last ann
CDKN2 PROTEIN (FRAGMENT).
Q9EQ33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).
Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weaver-Feldhaus J., Kamb A., Bergman W., Frants R.R.;
"Homozygotes for CNR2 (p16) germline mutation in Dutch familial melanoma kindreds.";
Nat. Genet. 10:351-553(1995).
SEQUENCE 21 AA; 2192 MW; 9424A5E1D7DEAFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                           ANK repeat; Repeat.
NON_TER 144
SEQUENCE 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; A7291998; AA659801.1; -. EMBL; A7291997; AA659801.1; JOINED. HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muscarella P., Knobloch T.J., Weghorst C.M.;
"Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and Identification of Inactivating Alterations in Hamster Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruis N.A., van der Velden P.A., Sandkuijl L.A.,
Weaver-Feldhaus J., Kamb A., Bergman W., Frants
                                                                                                                                                                                                                                                                                                                               SMART; SM00248; ANK; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus
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                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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14; Conserv
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12; Conserv
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                                                                                                                                                                                     Conservative
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                               83
                                                                                                                                                83
                                                                                                                                                                                                                                                                               144
15206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.5%;
                                                                                                                                                                                                  8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                    Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; I Catarrhini; Hominidae;
                     PRT;
                                                                                                                                                                                                                                                                                8904F9C0C316A084 CRC64;
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                                                                                                                                                                                   Mismatches
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                     157
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0.0019;
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4.3e-06;
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                                                                                                                                                                                                                      Length 144;
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Gaps

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Gaps

01-MAR-2001 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.

16, 16,

Created)

Last sequence update)

Last annotation

update)

CYCLIN-DEPENDENT KINASE INHIBITOR 2. Mesocricetus auratus (Golden hamster)

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RESULT
Q9QUJ3
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Best Local S
Matches 8
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Best Local
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01-MAY-2000
01-DEC-2001
                                                                                                                                  Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U80415; AAD00358.1; -. EMBL; U80413; AAD00356.1; -. EMBL; U80414; AAD00357.1; -. Interpro; IPR002110; ANK. Pfam; PF00023; ank; 1. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-VARIOUS STRAINS;
Santos J., Melendez B., Perez de Castro I.,
                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002110; ANK.
SMART; SM00248; ANK; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL; AF292567; AAG44950.1; HSSP; P42771; 1BI7
                                                                                                           PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                         Malumbres M., Serrano M., Pellicer A., Fernar "Comparative analysis of the p16 (INK4a) and
                                                                                                                                                                                                                                                                                                                                                        CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                  292013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muscarella P., Knobloch T.J., Weghorst C.M.; "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and Identification of Inactivating Alterations in Hamster Tumor
                                                                              SEQUENCE
                                                                                         ANK repeat; Cyclin; NON_TER 44
                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                               Q9QUJ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lines."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 RPVHDAAREGFL 83
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 8
                                                                                                                                                                                                               mouse inbred strains."
                                                                                                                                                                                                                                                                                                                                                                                                                                     26
 LATAAARG 15
                      Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Kinase;
157 AA;
                                                                              44 AA;
                                                                                                                                                                                                                                                                                                                                                                 ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
                     5.4%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                              4537
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16635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                   Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%;
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                                                                              MW;
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13,
19,
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Last sequence update)
Last annotation update)
                      0;
                     Score 8; DB 1
Pred. No. 3.9
0; Mismatches
                                                                                                   Repeat.
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Pred. No.
                                                                              AFBBF6B347AB8B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06FD66AE6B30DCF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                        Fernandez-Piqueras
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0.002;
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                                11;
.9;
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                                          Length 44;
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                                                                                                                                                                                                                            (INK4b) DNA sequences
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                      Indels
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                    Gaps
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RESULT
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Best Local Similarity
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Best Local
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Q9WLJ9;
01-NOV-1999
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
0NONSTRUCTURAL POLYPROTEIN (FRACMENT)
                                                                                                 NON_TER
NON_TER
SEQUENCE
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Q9Z1C0;
                                                                                                                                                                                       MEDLINE=99013657; PubMed=9797311;
Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;
"Characterization of a strain of infectious hepatitis E vi
from sewage in an area where hepatitis E is not endemic.";
Appl. Environ. Microbiol. 64:4485-4488(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update
CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, NCBI_TaxID=12461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002110; ANK. Pfam; PF00023; ank; 1. SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malumbres M., Serrano M., Pellicer A., Fernar "Comparative analysis of the pl6 (INK4a) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutereoscomir; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                    STRAIN-BCN
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK_REPEAT; 1. PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases EMBL; U80416; AAD00359.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Santos J., Melendez B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus spretus (Western wild mouse).
                                                                                                                                                                      Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANK repeat; Kinase; Repeat.
NON_TER 44 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in mouse inbred strains."
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8; Conserv
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                                                                                                                           91
                                                                                                    AA;
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                                                                                                    10056 MW;
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           5.4%;
100.0%;
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, Pellicer A., Fernandez-Piqueras
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         Score
Pred.
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Pred. No.
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                                                                                                    9017B9EC0CBA3A43 CRC64;
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8;
No.
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         DB 12;
. 7.5;
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.9;
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                              Length 91;
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RESULT
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Best Local
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                                                                                                                                                                                                                                                            P70067;
01-FEB-1997 (TrEME
01-MAY-1999 (TrEME
01-DEC-2001 (TrEME
13CDKN2X PROTEIN.
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Q9W618;
01-NOV-1999
                                                                                                                                                         Xiphophorus maculatus (Southern platyfish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Cyprinodontiformes; Poeciliidae; Xiphophorus.
                                         SEQUENCE OF 47-80 FROM N.A. STRAIN-JP 163 A; TISSUE-MUSCLE; STRAIN-JP 163 A; TISSUE-MUSCLE; MEDLINE-97075115; PubMed-8917541; Nairn R.S., Kazianis S., McEntire Morizot D.C.;
                                                                                                                                                                                                                                                CDNK2X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kazianis S., Morizot D.C., Della Coletta L., Woolcock B., Vielkind J.R., Nairn R.S.; Woolcock B., Vielkind J.R., Nairn R.S.; "Comparative Structure and Characterization Xiphophorus Fish Melanoma Model."; Submitted (MAR-1999) to the EMBL/GenBank/DDB EMBL, 8f125500; ADD1313.1; -...
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Best Local
                                                       MEDLINE-92113549; PubMed-1662697; McGeoch D.J., Cunningham C., McInt "Comparative sequence analysis of adjoining parts of the long unique simplex viruses types 1 and 2."; J. Gen. Virol. 72:3057-3075(1991).
                                                                                                                                                                                                            "Comparative DNA sequence analysis of different strains of herpes simplex a truncated UL41 product.",
J. Gen. Virol. 71:1387-1390(1990).
        STRAIN-HG52;
                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HG52;
MEDLINE-87111457; PubMed-3027242;
MCGeoch D.J., Moss H.W., McNab D., Frame M.C.;
MCGeoch D.J., Moss H.W., McNab D., Frame M.C.;
MNA sequence and genetic content of the HindIII 1 region in unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutions.
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Viruses; dsDNA viruse
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"Comparative Structure and Characterization of a CDKN2 Gene Xiphophorus Fish Melanoma Model.";
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Woolcock B.,
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